

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Maertens, Geert  
Bosmar, Fons  
De Martynoff, Guy  
Buyse, Marie-Ange
- (ii) TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.
- (iii) NUMBER OF SEQUENCES: 122
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: NIXON & VANDERHYE  
(B) STREET: 1100 North Glebe Road, 8th Floor  
(C) CITY: Arlington, VA 22201  
(E) COUNTRY: USA  
(F) ZIP: 22201
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DCS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: Unassigned  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Sadoff, B. J.  
(B) REGISTRATION NUMBER: 36663  
(C) REFERENCE/DOCKET NUMBER: 2551-61
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (703) 816-4000  
(B) TELEFAX: (703) 816-4100

## (2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCATGCAAG CTTAATTAAT T

21

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CCGGGGAGGC CTGCACGTGA TCGAGGGCAG ACACCATCAC CACCATCACT AATAGTTAAT  
 TAACTGCA

60

68

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 642 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..639

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA CTG TCC TGT  
 Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys  
 1 5 10 15

48

CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG TCC GGG ATG  
 Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met  
 20 25 30

96

TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA  
 Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala

144

35	40	45	
GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu 50 55 60			192
AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG CTC GCA GCT Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala 65 70 75 80			240
AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC GTC GAT TTG Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu 85 90 95			288
CTC GTT GGG GCG GCT GCT CTC TGT TCC GCT ATG TAC GTG GGG GAT CTC Leu Val Gly Ala Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu 100 105 110			336
TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC TCG CCT CGC Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg 115 120 125			384
CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His 130 135 140			432
ATA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro 145 150 155 160			480
ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val 165 170 175			528
GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala 180 185 190			576
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu 195 200 205			624
CTC TTT GCT CTC TAATAG Leu Phe Ala Leu 210			642

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys
1				5					10					15	
Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Met

20										25										30																																
Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala																																					
		35						40					45																																							
Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu																																					
		50				55					60																																									
Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala																																					
		65			70					75																																										
Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu																																					
				85					90					95																																						
Leu	Val	Gly	Ala	Ala	Ala	Leu	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu																																					
			100					105					110																																							
Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg																																					
		115					120					125																																								
Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His																																					
						135					140																																									
Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro																																					
		145				150				155																																										
Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val																																					
				165					170					175																																						
Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala																																					
			180					185					190																																							
Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Ile	Val	Met	Leu																																					
		195					200					205																																								
Leu	Phe	Ala	Leu																																																	
		210																																																		

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 795 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..792

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATG Met 1	TTG Leu	GGT Gly	AAG Lys	GTC Val 5	ATC Ile	GAT Asp	ACC Thr	CTT Leu	ACA Thr 10	TGC Cys	GGC Gly	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu	48
GTG Val	GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala 25	CCC Pro	CTA Leu	GGG Gly	GGC Gly	GCT Ala 30	GCC Ala	AGG Arg	96
GCC Ala	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAG Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144
ACA Thr	GGG Gly 50	AAT Asn	TTG Leu	CCC Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTG Leu	192
CTG Leu 65	TCC Ser	TGT Cys	CTG Leu	ACC Thr	GTT Val 70	CCA Pro	GCT Ala	TCC Ser	GCT Ala 75	TAT Tyr	GAA Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	240
TCC Ser	GGG Gly	ATG Met	TAC Tyr	CAT His 85	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys 90	TCC Ser	AAC Asn	TCA Ser	AGC Ser	ATT Ile 95	GTG Val	288
TAT Tyr	GAG Glu	GCA Ala 100	GCG Ala	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys	336
GTT Val	CGG Arg 115	GAG Glu	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala 125	CTC Leu	ACC Thr	CCC Pro	ACG Thr	384
CTC Leu 130	GCA Ala	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	GTC Val	CCC Pro	ACC Thr	ACG Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	432
GTC Val 145	GAT Asp	TTG Leu	CTC Leu	GTT Val 150	GGG Gly	GCG Ala	GCT Ala	GCT Ala	TTC Phe	TGT Cys 155	TCC Ser	GCT Ala	ATG Met	TAC Tyr	GTG Val 160	480
GGG Gly	GAC Asp	CTC Leu	TGC Cys 165	GGA Gly	TCT Ser	GTC Val	TTC Phe	CTC Leu	GTC Val 170	TCC Ser	CAG Gln	CTG Leu	TTC Phe 175	ACC Thr	ATC Ile	528
TCG Ser	CCT Pro	CGC Arg	CGG Arg 180	CAT His	GAG Glu	ACG Thr	GTG Val	CAG Gln 185	GAC Asp	TGC Cys	AAT Asn	TGC Cys	TCA Ser 190	ATC Ile	TAT Tyr	576
CCC Pro	GGC Gly 195	CAC His	ATA Ile	ACG Thr	GGT Gly	CAC His	CGT Arg 200	ATG Met	GCT Ala	TGG Trp	GAT Asp 205	ATG Met	ATG Met	ATG Met	AAC Asn	624
TGG Trp 210	TCG Ser	CCT Pro	ACA Thr	ACG Thr	GCC Ala	CTG Leu 215	GTG Val	GTA Val	TCG Ser	CAG Gln 220	CTG Leu	CTC Leu	CGG Arg	ATC Ile	CCA Pro	672
CAA Gln 225	GCT Ala	GTC Val	GTG Val	GAC Asp	ATG Met 230	GTG Val	GCG Ala	GGG Gly	GCC Ala 235	CAT His	TGG Trp	GGA Gly	GTC Val	CTG Leu	GCG Ala 240	720
GGT	CTC	GCC	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	768

Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile  
 245 250 255

GTG ATG CTA CTC TTT GCT CCC TAATAG  
 Val Met Leu Leu Phe Ala Pro  
 260

795

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 263 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu  
 1 5 10 15  
 Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg  
 20 25 30  
 Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala  
 35 40 45  
 Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu  
 50 55 60  
 Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val  
 65 70 75 80  
 Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val  
 85 90 95  
 Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys  
 100 105 110  
 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr  
 115 120 125  
 Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His  
 130 135 140  
 Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val  
 145 150 155 160  
 Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile  
 165 170 175  
 Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr  
 180 185 190  
 Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn  
 195 200 205  
 Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro  
 210 215 220  
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala

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225                      230                      235                      240
Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile
                245                      250                      255
Val Met Leu Leu Phe Ala Pro
                260

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(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 633 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..630

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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ATG TTG GGT AAG GTC ATC GAT ACC CTT ACG TGC GGC TTC GCC GAC CTC      48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
  1                      5                      10                      15

ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGT GCT GCC AGA      96
Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
                20                      25                      30

GCC CTG GCG CAT GGC GTC CGG GTT CTG GAA GAC GGC GTG AAC TAT GCA      144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
                35                      40                      45

ACA GGG AAT TTG CCT GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA      192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
                50                      55                      60

CTG TCC TGT CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG      240
Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
        65                      70                      75                      80

TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG      288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
                85                      90                      95

TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC      336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
                100                      105                      110

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(2) INFORMATION FOR SEO ID NO: 8:

(A) LENGTH: 209 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
1				5					10					15	
Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
			20					25					30		
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala
		35					40					45			
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
	50					55					60				
Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
65					70					75					80
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		



(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 483 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..480

(ix) FEATURE:  
(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 1..477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATG	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCC	CTG	CTG	TCC	TGT
Met	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys
1				5					10					15	
CTG	ACC	ATA	CCA	GCT	TCC	GCT	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG
Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val
			20					25					30		
TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATA	GTG	TAT	GAG	GCA
Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala
		35					40					45			
CGC	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	CGG	GAG
Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu
		50				55						60			

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..480

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 1..477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATG	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCC	CTG	CTG	TCC	TGT	48
Met	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	
1				5					10					15		
CTG	ACC	ATA	CCA	GCT	TCC	GCT	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	96
Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	
			20					25					30			
TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATA	GTG	TAT	GAG	GCA	144
Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	
		35				40						45				
GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	CGG	GAG	192
Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	
	50					55					60					

(2) INFORMATION FOR SEQ ID NO: 10:

(A) LENGTH: 159 amino acids

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Ala	Leu	Leu	Ser	Cys	1	5	10	15
Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	20	25	30
Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	35	40	45
Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	50	55	60
Gly	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	65	70	75
Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	85	90	95
Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	100	105	110
Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	115	120	125
Arg	His	Gln	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His			

(2) INFORMATION FOR SEQ ID NO: 11:

(ii) MOLECULE TYPE: cDNA

(iii) ANTI-SENSE: NO

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(ix) FEATURE:
      (A) NAME/KEY: mat_peptide
      (B) LOCATION: 1..474
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATG	TCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCC	CTG	CTG	TCC	TGT	48
Met	Ser	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	
1				5					10					15		
CTG	ACC	ATA	CCA	GCT	TCC	GCT	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	96
Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	
			20					25					30			
TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATA	GTG	TAT	GAG	GCA	144
Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	
		35					40					45				
GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	CGG	GAG	192
Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	
	50					55					60					
GGC	AAC	TCC	TCC	CGT	TGC	TGG	GTG	GCG	CTC	ACT	CCC	ACG	CTC	GCG	GCC	240
Gly	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	
65					70					75					80	
AGG	AAC	GCC	AGC	GTC	CCC	ACA	ACG	ACA	ATA	CGA	CGC	CAC	GTC	GAT	TTG	288
Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	
				85					90					95		
CTC	GTT	GGG	GCT	GCT	GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	336
Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	
			100					105					110			
TGC	GGA	TCT	GTT	TTC	CTT	GTT	TCC	CAG	CTG	TTC	ACC	TTC	TCA	CCT	CGC	384
Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	

(2) INFORMATION FOR SEO ID NO: 12:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

(2) INFORMATION FOR SEO ID NO: 13:

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..633

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATG	CTG	GGT	AAG	GCC	ATC	GAT	ACC	CTT	ACG	TGC	GGC	TTC	GCC	GAC	CTC	48
Met	Leu	Gly	Lys	Ala	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	
1				5					10					15		
GTG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	CTA	GGG	GGC	GCT	GCC	AGG	96
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	
			20					25					30			
GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	144
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	
		35					40					45				
ACA	GGG	AAT	TTG	CCT	GGT	TGC	TCT	CTC	TCT	ATC	TTC	CTC	TTG	GCT	TTA	192
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	
	50					55					60					
CTG	TCC	TGT	CTA	ACC	ATT	CCA	GCT	TCC	GCT	TAC	GAG	GTG	CGC	AAC	GTG	240
Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	
65					70					75					80	
TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	288
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	
				85					90					95		
TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	336
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	
			100					105					110			
GTT	CGG	GAG	AAC	AAC	TCT	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACC	CCC	ACG	384
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	
		115					120					125				
CTC	GCG	GCT	AGG	AAC	GCC	AGC	ATC	CCC	ACT	ACA	ACA	ATA	CGA	CGC	CAC	432
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Ile	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	
		130					135					140				
GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	480
Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	
145					150					155					160	
GGG	GAT	CTC	TGC	GGA	TCT	GTC	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	ATC	528
Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	
				165					170					175		
TCG	CCT	CGC	CGG	CAT	GAG	ACG	GTG	CAG	GAC	TGC	AAT	TGC	TCA	ATC	TAT	576
Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	

180	185	190	
CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC			624
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn			
195	200	205	
TGG TAC TAATAG			640
Trp Tyr			
210			

## (2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 210 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met	Leu	Gly	Lys	Ala	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
1				5					10					15	
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
			20					25					30		
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala
		35					40					45			
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
		50				55					60				
Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
	65				70					75					80
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85				90						95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr
			115					120				125			
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Ile	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His
			130				135					140			
Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val
	145				150					155					160
Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile
			165						170					175	
Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr
			180					185					190		
Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn
		195					200					205			

(2) INFORMATION FOR SEQ ID NO: 15:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

26

(2) INFORMATION FOR SEQ ID NO: 16:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

26

(2) INFORMATION FOR SEQ ID NO: 17:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CTATTAGGAC CAGTTCATCA TCATATCCCA

30

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CTATTACCAG TTCATCATCA TATCCCA

27

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATACGACGCC ACGTCGATTC CCAGCTGTTC ACCATC

36

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GATGGTGAAC AGCTGGGAAT CGACGTGGCG TCGTAT

36

(2) INFORMATION FOR SEQ ID NO: 21:

CTATTAGGAC CAGTTCATCA TCATATCCCA



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 723 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..720

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG	480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	

145		150		155		160	
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT							528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg							
		165		170		175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG							576
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val							
		180		185		190	
GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG							624
Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala							
		195		200		205	
GGG GCC CAT TGG GGA GTC CTG GCG GGT CTC GCC TAC TAT TCC ATG GTG							672
Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val							
		210		215		220	
GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA CTC TTT GCT CCC TAATAG							723
Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro							
		225		230		235	240

## (2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 239 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
1				5					10					15	
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
		20						25					30		
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala
		35					40					45			
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
		50				55				60					
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
		65			70					75				80	
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
			85						90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
		100						105					110		
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr
		115					120					125			
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His
		130					135					140			
Val	Asp	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val

(2) INFORMATION FOR SEQ ID NO: 23:

(ii) MOLECULE TYPE: cDNA

(iii) ANTI-SENSE: NO

```
(ix) FEATURE:
      (A) NAME/KEY: mat_peptide
      (B) LOCATION: 1..555
```

ATG	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTT	ACA	TGC	GGC	TTC	GCC	GAC	CTC	48
Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	
1				5				10						15		
GTG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	CTA	GGG	GGC	GCT	GCC	AGG	96
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	
			20				25						30			
GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	144
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	
		35					40					45				
ACA	GGG	AAT	TTG	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTG	192
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	
	50					55					60					
CTG	TCC	TGT	CTG	ACC	GTT	CCA	GCT	TCC	GCT	TAT	GAA	GTG	CGC	AAC	GTG	240
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	

65	70	75	80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG				288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	85	90	95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC				336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	100	105	110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG				384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	115	120	125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC				432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	130	135	140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG				480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	145	150	155	160
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT				528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg	165	170	175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TAATAG				561
Met Ala Trp Asp Met Met Met Asn Trp	180	185		

## (2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 185 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	1	5	10	15
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	20	25	30	
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	35	40	45	
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	50	55	60	
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	65	70	75	80
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	85	90	95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	100	105	110	

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ATG	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTT	ACA	TGC	GGC	TTC	GCC	GAC	CTC	48
Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	
1				5					10					15		
GTG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	CTA	GGG	GGC	GCT	GCC	AGG	96
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	
			20					25					30			
GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	144
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	
		35					40					45				
ACA	GGG	AAT	TTG	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTG	192
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	
	50					55					60					
CTG	TCC	TGT	CTG	ACC	GTT	CCA	GCT	TCC	GCT	TAT	GAA	GTG	CGC	AAC	GTG	240
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	
65					70					75					80	

TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG	480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	
145 150 155 160	
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT	528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg	
165 170 175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG	576
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val	
180 185 190	
GTA TCG CAG CTG CTC CGG ATC CTC TAATAG	606
Val Ser Gln Leu Leu Arg Ile Leu	
195 200	

## (2) INFORMATION FOR SEQ ID NO: 26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
1				5					10					15	
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
		20						25					30		
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala
		35					40					45			
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
	50					55					60				
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
	65				70					75				80	
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	

(2) INFORMATION FOR SEQ ID NO: 27:

- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- ```
(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 1..633

(ix) FEATURE:
      (A) NAME/KEY: mat_peptide
      (B) LOCATION: 1..630
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | TTG | GGT | AAG | GTC | ATC | GAT | ACC | CTT | ACA | TGC | GGC | TTC | GCC | GAC | CTC | 48  |
| Met | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GTG | GGG | TAC | ATT | CCG | CTC | GTC | GGC | GCC | CCC | CTA | GGG | GGC | GCT | GCC | AGG | 96  |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GCC | CTG | GCG | CAT | GGC | GTC | CGG | GTT | CTG | GAG | GAC | GGC | GTG | AAC | TAT | GCA | 144 |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| ACA | GGG | AAT | TTG | CCC | GGT | TGC | TCT | TTT | TCT | ATC | TTC | CTC | TTG | GCT | TTG | 192 |

```

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
  50                      55                      60

CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG      240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
  65                      70                      75                      80

TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG      288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
                      85                      90                      95

TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC      336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
                      100                      105                      110

GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG      384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
                      115                      120                      125

CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC      432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
                      130                      135                      140

GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG      480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val
                      145                      150                      155                      160

CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT      528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
                      165                      170                      175

ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG      576
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val
                      180                      185                      190

GTA TCG CAG CTG CTC CGG ATC GTG ATC GAG GGC AGA CAC CAT CAC CAC      624
Val Ser Gln Leu Leu Arg Ile Val Ile Glu Gly Arg His His His His
                      195                      200                      205

CAT CAC TAATAG
His His
  210

```

## (2) INFORMATION FOR SEQ ID NO: 28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
  1                      5                      10                      15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
  20                      25                      30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala

```



(2) INFORMATION FOR SEQ ID NO: 29:

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

48

(2) INFORMATION FOR SEQ ID NO: 30:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met  
 1 5 10 15

Gly Tyr Ile Pro Leu Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala  
 20 25 30

Leu Ala His Gly Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr  
 35 40 45

Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe  
 50 55 60

Ser Cys Leu Ile His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser  
 65 70 75 80

Gly Leu Tyr Val Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr  
 85 90 95

Glu Ala Asp Asp Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val  
 100 105 110

Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val  
 115 120 125

Ala Val Lys Tyr Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val  
 130 135 140

Asp Leu Leu Val Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly  
 145 150 155 160

Asp Met Cys Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg  
 165 170 175

Pro Arg Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro  
 180 185 190

Gly His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
 195 200 205

## (2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 630 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..627

## (ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 1..624

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC GCC GAT CTC ATG | 48  |
| Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met |     |
| 1 5 10 15                                                       |     |
| GGG TAT ATC CCG CTC GTA GGC GGC CCC ATT GGG GGC GTC GCA AGG GCT | 96  |
| Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile Gly Gly Val Ala Arg Ala |     |
| 20 25 30                                                        |     |
| CTC GCA CAC GGT GTG AGG GTC CTT GAG GAC GGG GTA AAC TAT GCA ACA | 144 |
| Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr |     |
| 35 40 45                                                        |     |
| GGG AAT TTA CCC GGT TGC TCT TTC TCT ATC TTT ATT CTT GCT CTT CTC | 192 |
| Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu |     |
| 50 55 60                                                        |     |
| TCG TGT CTG ACC GTT CCG GCC TCT GCA GTT CCC TAC CGA AAT GCC TCT | 240 |
| Ser Cys Leu Thr Val Pro Ala Ser Ala Val Pro Tyr Arg Asn Ala Ser |     |
| 65 70 75 80                                                     |     |
| GGG ATT TAT CAT GTT ACC AAT GAT TGC CCA AAC TCT TCC ATA GTC TAT | 288 |
| Gly Ile Tyr His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr |     |
| 85 90 95                                                        |     |
| GAG GCA GAT AAC CTG ATC CTA CAC GCA CCT GGT TGC GTG CCT TGT GTC | 336 |
| Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val |     |
| 100 105 110                                                     |     |
| ATG ACA GGT AAT GTG AGT AGA TGC TGG GTC CAA ATT ACC CCT ACA CTG | 384 |
| Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu |     |
| 115 120 125                                                     |     |
| TCA GCC CCG AGC CTC GGA GCA GTC ACG GCT CCT CTT CGG AGA GCC GTT | 432 |
| Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val |     |
| 130 135 140                                                     |     |
| GAC TAC CTA GCG GGA GGG GCT GCC CTC TGC TCC GCG TTA TAC GTA GGA | 480 |
| Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly |     |
| 145 150 155 160                                                 |     |
| GAC GCG TGT GGG GCA CTA TTC TTG GTA GGC CAA ATG TTC ACC TAT AGG | 528 |
| Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg |     |
| 165 170 175                                                     |     |
| CCT CGC CAG CAC GCT ACG GTG CAG AAC TGC AAC TGT TCC ATT TAC AGT | 576 |
| Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser |     |
| 180 185 190                                                     |     |
| GGC CAT GTT ACC GGC CAC CGG ATG GCA TGG GAT ATG ATG ATG AAC TGG | 624 |
| Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp |     |
| 195 200 205                                                     |     |

TAATAG

630

## (2) INFORMATION FOR SEQ ID NO: 32:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu | Met | 1   | 5   | 10  | 15  |
| Gly | Tyr | Ile | Pro | Leu | Val | Gly | Gly | Pro | Ile | Gly | Gly | Val | Ala | Arg | Ala | 20  | 25  | 30  |     |
| Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala | Thr | 35  | 40  | 45  |     |
| Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Ile | Leu | Ala | Leu | Leu | 50  | 55  | 60  |     |
| Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Val | Pro | Tyr | Arg | Asn | Ala | Ser | 65  | 70  | 75  | 80  |
| Gly | Ile | Tyr | His | Val | Thr | Asn | Asp | Cys | Pro | Asn | Ser | Ser | Ile | Val | Tyr | 85  | 90  | 95  |     |
| Glu | Ala | Asp | Asn | Leu | Ile | Leu | His | Ala | Pro | Gly | Cys | Val | Pro | Cys | Val | 100 | 105 | 110 |     |
| Met | Thr | Gly | Asn | Val | Ser | Arg | Cys | Trp | Val | Gln | Ile | Thr | Pro | Thr | Leu | 115 | 120 | 125 |     |
| Ser | Ala | Pro | Ser | Leu | Gly | Ala | Val | Thr | Ala | Pro | Leu | Arg | Arg | Ala | Val | 130 | 135 | 140 |     |
| Asp | Tyr | Leu | Ala | Gly | Gly | Ala | Ala | Leu | Cys | Ser | Ala | Leu | Tyr | Val | Gly | 145 | 150 | 155 | 160 |
| Asp | Ala | Cys | Gly | Ala | Leu | Phe | Leu | Val | Gly | Gln | Met | Phe | Thr | Tyr | Arg | 165 | 170 | 175 |     |
| Pro | Arg | Gln | His | Ala | Thr | Val | Gln | Asn | Cys | Asn | Cys | Ser | Ile | Tyr | Ser | 180 | 185 | 190 |     |
| Gly | His | Val | Thr | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn | Trp | 195 | 200 | 205 |     |

## (2) INFORMATION FOR SEQ ID NO: 33:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

```
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
```

23

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
```

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
```

```
(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 1..1473

(ix) FEATURE:
      (A) NAME/KEY: mat_peptide
      (B) LOCATION: 1..1470
```

48

|                   |                   |                   |                   |                   |            |                   |                   |                   |                   |                   |                   |                   |                  |                   |                   |     |
|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|-----|
| Trp<br>1          | Asp               | Met               | Met               | Met<br>5          | Asn        | Trp               | Ser               | Pro               | Thr<br>10         | Ala               | Leu               | Val               | Val<br>15        | Ser               |                   |     |
| CAG<br>Gln        | CTG<br>Leu        | CTC<br>Leu        | CGG<br>Arg<br>20  | ATC<br>Ile        | CCA<br>Pro | CAA<br>Gln        | GCT<br>Ala        | GTC<br>Val<br>25  | GTG<br>Val        | GAC<br>Asp        | ATG<br>Met        | GTG<br>Val        | GCG<br>Ala<br>30 | GGG<br>Gly        | GCC<br>Ala        | 96  |
| CAT<br>His        | TGG<br>Trp        | GGA<br>Gly<br>35  | GTC<br>Val        | CTG<br>Leu        | GCG<br>Ala | GGC<br>Gly        | CTC<br>Leu<br>40  | GCC<br>Ala        | TAC<br>Tyr        | TAT<br>Tyr        | TCC<br>Ser        | ATG<br>Met<br>45  | GTG<br>Val       | GGG<br>Gly        | AAC<br>Asn        | 144 |
| TGG<br>Trp        | GCT<br>Ala<br>50  | AAG<br>Lys        | GTT<br>Val        | TTG<br>Leu        | GTT<br>Val | GTG<br>Val<br>55  | ATG<br>Met        | CTA<br>Leu        | CTC<br>Leu        | TTT<br>Phe        | GCC<br>Ala<br>60  | GGC<br>Gly        | GTC<br>Val       | GAC<br>Asp        | GGG<br>Gly        | 192 |
| CAT<br>His<br>65  | ACC<br>Thr        | CGC<br>Arg        | GTG<br>Val        | TCA<br>Ser<br>70  | GGA<br>Gly | GGG<br>Gly        | GCA<br>Ala        | GCA<br>Ala        | GCC<br>Ala        | TCC<br>Ser<br>75  | GAT<br>Asp        | ACC<br>Thr        | AGG<br>Arg       | GGC<br>Gly        | CTT<br>Leu<br>80  | 240 |
| GTG<br>Val        | TCC<br>Ser        | CTC<br>Leu        | TTT<br>Phe        | AGC<br>Ser<br>85  | CCC<br>Pro | GGG<br>Gly        | TCG<br>Ser        | GCT<br>Ala        | CAG<br>Gln<br>90  | AAA<br>Lys        | ATC<br>Ile        | CAG<br>Gln        | CTC<br>Leu       | GTA<br>Val<br>95  | AAC<br>Asn        | 288 |
| ACC<br>Thr        | AAC<br>Asn        | GGC<br>Gly        | AGT<br>Ser<br>100 | TGG<br>Trp        | CAC<br>His | ATC<br>Ile        | AAC<br>Asn<br>105 | AGG<br>Thr        | ACT<br>Ala        | GCC<br>Leu        | CTG<br>Asn        | AAC<br>Cys<br>110 | TGC<br>Asn       | AAC<br>Asp        | GAC<br>Asp        | 336 |
| TCC<br>Ser        | CTC<br>Leu<br>115 | CAA<br>Gln        | ACA<br>Thr        | GGG<br>Gly        | TTC<br>Phe | TTT<br>Phe        | GCC<br>Ala<br>120 | GCA<br>Ala        | CTA<br>Leu        | TTC<br>Phe        | TAC<br>Tyr        | AAA<br>Lys<br>125 | CAC<br>His       | AAA<br>Lys        | TTC<br>Phe        | 384 |
| AAC<br>Asn<br>130 | TCG<br>Ser        | TCT<br>Ser        | GGA<br>Gly        | TGC<br>Cys        | CCA<br>Pro | GAG<br>Glu<br>135 | CGC<br>Arg        | TTG<br>Leu        | GCC<br>Ala        | AGC<br>Ser        | TGT<br>Cys<br>140 | CGC<br>Arg        | TCC<br>Ser       | ATC<br>Ile        | GAC<br>Asp        | 432 |
| AAG<br>Lys<br>145 | TTC<br>Phe        | GCT<br>Ala        | CAG<br>Gln        | GGG<br>Gly<br>150 | TGG<br>Trp | GGT<br>Gly        | CCC<br>Pro        | CTC<br>Leu        | ACT<br>Thr<br>155 | TAC<br>Tyr        | ACT<br>Thr        | GAG<br>Glu        | CCT<br>Pro       | AAC<br>Asn        | AGC<br>Ser<br>160 | 480 |
| TCG<br>Ser        | GAC<br>Asp        | CAG<br>Gln        | AGG<br>Arg<br>165 | CCC<br>Pro        | TAC<br>Tyr | TGC<br>Cys        | TGG<br>Trp        | CAC<br>His<br>170 | TAC<br>Tyr        | GCG<br>Ala        | CCT<br>Pro        | CGA<br>Arg        | CCG<br>Pro       | TGT<br>Cys<br>175 | GGT<br>Gly        | 528 |
| ATT<br>Ile        | GTA<br>Val        | CCC<br>Pro<br>180 | GCG<br>Ala        | TCT<br>Ser        | CAG<br>Gln | GTG<br>Val        | TGC<br>Cys<br>185 | GGT<br>Gly        | CCA<br>Pro        | GTG<br>Val        | TAT<br>Tyr        | TGC<br>Cys<br>190 | TTC<br>Phe       | ACC<br>Thr        | CCG<br>Pro        | 576 |
| AGC<br>Ser        | CCT<br>Pro<br>195 | GTT<br>Val        | GTG<br>Val        | GGG<br>Gly        | ACG<br>Thr | ACC<br>Thr<br>200 | GAT<br>Asp        | CGG<br>Arg        | TTT<br>Phe        | GGT<br>Gly        | GTC<br>Val<br>205 | CCC<br>Pro        | ACG<br>Thr       | TAT<br>Tyr        |                   | 624 |
| AAC<br>Asn<br>210 | TGG<br>Trp        | GGG<br>Gly        | GCG<br>Ala        | AAC<br>Asn        | GAC<br>Asp | TCG<br>Ser<br>215 | GAT<br>Asp        | GTG<br>Val        | CTG<br>Leu        | ATT<br>Ile        | CTC<br>Leu<br>220 | AAC<br>Asn        | AAC<br>Asn       | ACG<br>Thr        | CGG<br>Arg        | 672 |
| CCG<br>Pro<br>225 | CCG<br>Pro        | CGA<br>Arg        | GGC<br>Gly        | AAC<br>Asn<br>230 | TGG<br>Trp | TTC<br>Phe        | GGC<br>Gly        | TGT<br>Cys        | ACA<br>Thr        | TGG<br>Trp<br>235 | ATG<br>Met        | AAT<br>Asn        | GGC<br>Gly       | ACT<br>Thr        | GGG<br>Gly<br>240 | 720 |
| TTC<br>Phe        | ACC<br>Thr        | AAG<br>Lys        | ACG<br>Thr<br>245 | TGT<br>Cys        | GGG<br>Gly | GGC<br>Gly        | CCC<br>Pro        | CCG<br>Pro<br>250 | TGC<br>Cys        | AAC<br>Asn        | ATC<br>Ile        | GGG<br>Gly        | GGG<br>Gly       | GCC<br>Ala<br>255 | GGC<br>Gly        | 768 |

|     |     |     |     |     |     |     |     |     |     |        |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--------|-----|-----|-----|-----|-----|------|
| AAC | AAC | ACC | TTG | ACC | TGC | CCC | ACT | GAC | TGT | TTT    | CGG | AAG | CAC | CCC | GAG | 816  |
| Asn | Asn | Thr | Leu | Thr | Cys | Pro | Thr | Asp | Cys | Phe    | Arg | Lys | His | Pro | Glu |      |
|     |     |     | 260 |     |     |     |     | 265 |     |        |     |     | 270 |     |     |      |
| GCC | ACC | TAC | GCC | AGA | TGC | GGT | TCT | GGG | CCC | TGG    | CTG | ACA | CCT | AGG | TGT | 864  |
| Ala | Thr | Tyr | Ala | Arg | Cys | Gly | Ser | Gly | Pro | Trp    | Leu | Thr | Pro | Arg | Cys |      |
|     |     |     | 275 |     |     |     | 280 |     |     |        |     | 285 |     |     |     |      |
| ATG | GTT | CAT | TAC | CCA | TAT | AGG | CTC | TGG | CAC | TAC    | CCC | TGC | ACT | GTC | AAC | 912  |
| Met | Val | His | Tyr | Pro | Tyr | Arg | Leu | Trp | His | Tyr    | Pro | Cys | Thr | Val | Asn |      |
|     | 290 |     |     |     |     | 295 |     |     |     |        | 300 |     |     |     |     |      |
| TTC | ACC | ATC | TTC | AAG | GTT | AGG | ATG | TAC | GTG | GGG    | GGC | GTG | GAG | CAC | AGG | 960  |
| Phe | Thr | Ile | Phe | Lys | Val | Arg | Met | Tyr | Val | Gly    | Gly | Val | Glu | His | Arg |      |
| 305 |     |     |     |     | 310 |     |     |     |     | 315    |     |     |     |     | 320 |      |
| TTC | GAA | GCC | GCA | TGC | AAT | TGG | ACT | CGA | GGA | GAG    | CGT | TGT | GAC | TTG | GAG | 1008 |
| Phe | Glu | Ala | Ala | Cys | Asn | Trp | Thr | Arg | Gly | Glu    | Arg | Cys | Asp | Leu | Glu |      |
|     |     |     |     | 325 |     |     |     |     | 330 |        |     |     |     | 335 |     |      |
| GAC | AGG | GAT | AGA | TCA | GAG | CTT | AGC | CCG | CTG | CTG    | CTG | TCT | ACA | ACA | GAG | 1056 |
| Asp | Arg | Asp | Arg | Ser | Glu | Leu | Ser | Pro | Leu | Leu    | Leu | Ser | Thr | Thr | Glu |      |
|     |     |     | 340 |     |     |     |     | 345 |     |        |     |     | 350 |     |     |      |
| TGG | CAG | ATA | CTG | CCC | TGT | TCC | TTC | ACC | ACC | CTG    | CCG | GCC | CTA | TCC | ACC | 1104 |
| Trp | Gln | Ile | Leu | Pro | Cys | Ser | Phe | Thr | Thr | Leu    | Pro | Ala | Leu | Ser | Thr |      |
|     |     |     | 355 |     |     |     | 360 |     |     |        |     | 365 |     |     |     |      |
| GGC | CTG | ATC | CAC | CTC | CAT | CAG | AAC | ATC | GTG | GAC    | GTG | CAA | TAC | CTG | TAC | 1152 |
| Gly | Leu | Ile | His | Leu | His | Gln | Asn | Ile | Val | Asp    | Val | Gln | Tyr | Leu | Tyr |      |
|     | 370 |     |     |     |     | 375 |     |     |     |        | 380 |     |     |     |     |      |
| GGT | GTA | GGG | TCG | GCG | GTT | GTC | TCC | CTT | GTC | ATC    | AAA | TGG | GAG | TAT | GTC | 1200 |
| Gly | Val | Gly | Ser | Ala | Val | Val | Ser | Leu | Val | Ile    | Lys | Trp | Glu | Tyr | Val |      |
| 385 |     |     |     |     | 390 |     |     |     |     | 395    |     |     |     |     | 400 |      |
| CTG | TTG | CTC | TTC | CTT | CTC | CTG | GCA | GAC | GCG | CGC    | ATC | TGC | GCC | TGC | TTA | 1248 |
| Leu | Leu | Leu | Phe | Leu | Leu | Leu | Ala | Asp | Ala | Arg    | Ile | Cys | Ala | Cys | Leu |      |
|     |     |     |     | 405 |     |     |     |     | 410 |        |     |     |     | 415 |     |      |
| TGG | ATG | ATG | CTG | CTG | ATA | GCT | CAA | GCT | GAG | GCC    | GCC | TTA | GAG | AAC | CTG | 1296 |
| Trp | Met | Met | Leu | Leu | Ile | Ala | Gln | Ala | Glu | Ala    | Ala | Leu | Glu | Asn | Leu |      |
|     |     |     | 420 |     |     |     |     | 425 |     |        |     |     | 430 |     |     |      |
| GTG | GTC | CTC | AAT | GCG | GCG | GCC | GTG | GCC | GGG | GCG    | CAT | GGC | ACT | CTT | TCC | 1344 |
| Val | Val | Leu | Asn | Ala | Ala | Ala | Val | Ala | Gly | Ala    | His | Gly | Thr | Leu | Ser |      |
|     |     |     | 435 |     |     |     | 440 |     |     |        |     | 445 |     |     |     |      |
| TTC | CTT | GTG | TTC | TTC | TGT | GCT | GCC | TGG | TAC | ATC    | AAG | GGC | AGG | CTG | GTC | 1392 |
| Phe | Leu | Val | Phe | Phe | Cys | Ala | Ala | Trp | Tyr | Ile    | Lys | Gly | Arg | Leu | Val |      |
|     | 450 |     |     |     |     | 455 |     |     |     |        | 460 |     |     |     |     |      |
| CCT | GGT | GCG | GCA | TAC | GCC | TTC | TAT | GGC | GTG | TGG    | CCG | CTG | CTC | CTG | CTT | 1440 |
| Pro | Gly | Ala | Ala | Tyr | Ala | Phe | Tyr | Gly | Val | Trp    | Pro | Leu | Leu | Leu | Leu |      |
| 465 |     |     |     |     | 470 |     |     |     |     | 475    |     |     |     |     | 480 |      |
| CTG | CTG | GCC | TTA | CCA | CCA | CGA | GCT | TAT | GCC | TAGTAA |     |     |     |     |     | 1476 |
| Leu | Leu | Ala | Leu | Pro | Pro | Arg | Ala | Tyr | Ala |        |     |     |     |     |     |      |
|     |     |     |     | 485 |     |     |     |     | 490 |        |     |     |     |     |     |      |



(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 490 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Asp | Met | Met | Met | Asn | Trp | Ser | Pro | Thr | Thr | Ala | Leu | Val | Val | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Leu | Leu | Arg | Ile | Pro | Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Trp | Gly | Val | Leu | Ala | Gly | Leu | Ala | Tyr | Tyr | Ser | Met | Val | Gly | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Trp | Ala | Lys | Val | Leu | Val | Val | Met | Leu | Leu | Phe | Ala | Gly | Val | Asp | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Thr | Arg | Val | Ser | Gly | Gly | Ala | Ala | Ala | Ser | Asp | Thr | Arg | Gly | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Ser | Leu | Phe | Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile | Gln | Leu | Val | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Asn | Gly | Ser | Trp | His | Ile | Asn | Arg | Thr | Ala | Leu | Asn | Cys | Asn | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Leu | Gln | Thr | Gly | Phe | Phe | Ala | Ala | Leu | Phe | Tyr | Lys | His | Lys | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Ser | Ser | Gly | Cys | Pro | Glu | Arg | Leu | Ala | Ser | Cys | Arg | Ser | Ile | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Phe | Ala | Gln | Gly | Trp | Gly | Pro | Leu | Thr | Tyr | Thr | Glu | Pro | Asn | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Asp | Gln | Arg | Pro | Tyr | Cys | Trp | His | Tyr | Ala | Pro | Arg | Pro | Cys | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Val | Pro | Ala | Ser | Gln | Val | Cys | Gly | Pro | Val | Tyr | Cys | Phe | Thr | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Pro | Val | Val | Val | Gly | Thr | Thr | Asp | Arg | Phe | Gly | Val | Pro | Thr | Tyr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Trp | Gly | Ala | Asn | Asp | Ser | Asp | Val | Leu | Ile | Leu | Asn | Asn | Thr | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Pro | Pro | Arg | Gly | Asn | Trp | Phe | Gly | Cys | Thr | Trp | Met | Asn | Gly | Thr | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Phe | Thr | Lys | Thr | Cys | Gly | Gly | Pro | Pro | Cys | Asn | Ile | Gly | Gly | Ala | Gly |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asn | Asn | Thr | Leu | Thr | Cys | Pro | Thr | Asp | Cys | Phe | Arg | Lys | His | Pro | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Thr | Tyr | Ala | Arg | Cys | Gly | Ser | Gly | Pro | Trp | Leu | Thr | Pro | Arg | Cys |

(2) INFORMATION FOR SEQ ID NO: 37:

(ii) MOLECULE TYPE: cDNA.

(iii) ANTI-SENSE: NO

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(ix) FEATURE:
      (A) NAME/KEY: mat_peptide
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| G   | ATC | CCA | CAA | GCT | GTC | GTG | GAC | ATG | GTG | GCG | GGG | GCC | CAT | TGG | GGA | 46  |
| Ile | Pro | Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His | Trp | Gly |     |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| GTC | CTG | GCG | GGC | CTC | GCC | TAC | TAT | TCC | ATG | GTG | GGG | AAC | TGG | GCT | AAG | 94  |
| Val | Leu | Ala | Gly | Leu | Ala | Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp | Ala | Lys |     |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| GTT | TTG | GTT | GTG | ATG | CTA | CTC | TTT | GCC | GGC | GTG | GAC | GGG | CAT | ACC | CGC | 142 |
| Val | Leu | Val | Val | Met | Leu | Leu | Phe | Ala | Gly | Val | Asp | Gly | His | Thr | Arg |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| GTG | TCA | GGA | GGG | GCA | GCA | GCC | TCC | GAT | ACC | AGG | GGC | CTT | GTG | TCC | CTC | 190 |
| Val | Ser | Gly | Gly | Ala | Ala | Ala | Ser | Asp | Thr | Arg | Gly | Leu | Val | Ser | Leu |     |
|     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| TTT | AGC | CCC | GGG | TCG | GCT | CAG | AAA | ATC | CAG | CTC | GTA | AAC | ACC | AAC | GGC | 238 |
| Phe | Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile | Gln | Leu | Val | Asn | Thr | Asn | Gly |     |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |     |
| AGT | TGG | CAC | ATC | AAC | AGG | ACT | GCC | CTG | AAC | TGC | AAC | GAC | TCC | CTC | CAA | 286 |
| Ser | Trp | His | Ile | Asn | Arg | Thr | Ala | Leu | Asn | Cys | Asn | Asp | Ser | Leu | Gln |     |
|     | 80  |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| ACA | GGG | TTC | TTT | GCC | GCA | CTA | TTC | TAC | AAA | CAC | AAA | TTC | AAC | TCG | TCT | 334 |
| Thr | Gly | Phe | Phe | Ala | Ala | Leu | Phe | Tyr | Lys | His | Lys | Phe | Asn | Ser | Ser |     |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| GGA | TGC | CCA | GAG | CGC | TTG | GCC | AGC | TGT | CGC | TCC | ATC | GAC | AAG | TTC | GCT | 382 |
| Gly | Cys | Pro | Glu | Arg | Leu | Ala | Ser | Cys | Arg | Ser | Ile | Asp | Lys | Phe | Ala |     |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| CAG | GGG | TGG | GGT | CCC | CTC | ACT | TAC | ACT | GAG | CCT | AAC | AGC | TCG | GAC | CAG | 430 |
| Gln | Gly | Trp | Gly | Pro | Leu | Thr | Tyr | Thr | Glu | Pro | Asn | Ser | Ser | Asp | Gln |     |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| AGG | CCC | TAC | TGC | TGG | CAC | TAC | GCG | CCT | CGA | CCG | TGT | GGT | ATT | GTA | CCC | 478 |
| Arg | Pro | Tyr | Cys | Trp | His | Tyr | Ala | Pro | Arg | Pro | Cys | Gly | Ile | Val | Pro |     |
|     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |
| GCG | TCT | CAG | GTG | TGC | GGT | CCA | GTG | TAT | TGC | TTC | ACC | CCG | AGC | CCT | GTT | 526 |
| Ala | Ser | Gln | Val | Cys | Gly | Pro | Val | Tyr | Cys | Phe | Thr | Pro | Ser | Pro | Val |     |
| 160 |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| GTG | GTG | GGG | ACG | ACC | GAT | CGG | TTT | GGT | GTC | CCC | ACG | TAT | AAC | TGG | GGG | 574 |
| Val | Val | Gly | Thr | Thr | Asp | Arg | Phe | Gly | Val | Pro | Thr | Tyr | Asn | Trp | Gly |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| GCG | AAC | GAC | TCG | GAT | GTG | CTG | ATT | CTC | AAC | AAC | ACG | CGG | CCG | CCG | CGA | 622 |
| Ala | Asn | Asp | Ser | Asp | Val | Leu | Ile | Leu | Asn | Asn | Thr | Arg | Pro | Pro | Arg |     |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| GGC | AAC | TGG | TTC | GGC | TGT | ACA | TGG | ATG |     |     |     |     |     |     |     |     |

| 225                                                             | 230 | 235 |      |
|-----------------------------------------------------------------|-----|-----|------|
| TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC |     |     | 766  |
| Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr |     |     |      |
| 240                                                             | 245 | 250 | 255  |
| GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT |     |     | 814  |
| Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His |     |     |      |
|                                                                 | 260 | 265 | 270  |
| TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC |     |     | 862  |
| Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile |     |     |      |
|                                                                 | 275 | 280 | 285  |
| TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC |     |     | 910  |
| Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala |     |     |      |
|                                                                 | 290 | 295 | 300  |
| GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT |     |     | 958  |
| Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp |     |     |      |
|                                                                 | 305 | 310 | 315  |
| AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GAG TGG CAG AGT |     |     | 1006 |
| Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ser |     |     |      |
|                                                                 | 320 | 325 | 330  |
| GGC AGA GCT TAATTA                                              |     |     | 1021 |
| Gly Arg Ala                                                     |     |     |      |

## (2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Pro | Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ala | Gly | Leu | Ala | Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp | Ala | Lys | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Val | Val | Met | Leu | Leu | Phe | Ala | Gly | Val | Asp | Gly | His | Thr | Arg | Val |
|     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ser | Gly | Gly | Ala | Ala | Ala | Ser | Asp | Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile | Gln | Leu | Val | Asn | Thr | Asn | Gly | Ser |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Trp | His | Ile | Asn | Arg | Thr | Ala | Leu | Asn | Cys | Asn | Asp | Ser | Leu | Gln | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Phe | Phe | Ala | Ala | Leu | Phe | Tyr | Lys | His | Lys | Phe | Asn | Ser | Ser | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln  
 115 120 125  
 Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg  
 130 135 140  
 Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala  
 145 150 155 160  
 Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val  
 165 170 175  
 Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala  
 180 185 190  
 Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly  
 195 200 205  
 Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr  
 210 215 220  
 Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu  
 225 230 235 240  
 Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala  
 245 250 255  
 Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr  
 260 265 270  
 Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe  
 275 280 285  
 Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala  
 290 295 300  
 Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg  
 305 310 315 320  
 Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ser Gly  
 325 330 335  
 Arg Ala

## (2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1034 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

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(ix) FEATURE:
      (A) NAME/KEY: mat_peptide
      (B) LOCATION: 2..1029
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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| G   | ATC | CCA | CAA | GCT | GTC | GTG | GAC | ATG | GTG | GCG | GGG | GCC | CAT | TGG | GGA | 46  |
| Ile | Pro | Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His | Trp | Gly |     |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |
| GTC | CTG | GCG | GGC | CTC | GCC | TAC | TAT | TCC | ATG | GTG | GGG | AAC | TGG | GCT | AAG | 94  |
| Val | Leu | Ala | Gly | Leu | Ala | Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp | Ala | Lys |     |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| GTT | TTG | GTT | GTG | ATG | CTA | CTC | TTT | GCC | GCG | GTG | GAC | GGG | CAT | ACC | CGC | 142 |
| Val | Leu | Val | Val | Met | Leu | Leu | Phe | Ala | Gly | Val | Asp | Gly | His | Thr | Arg |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| GTG | TCA | GGA | GGG | GCA | GCA | GCC | TCC | GAT | ACC | AGG | GGC | CTT | GTG | TCC | CTC | 190 |
| Val | Ser | Gly | Gly | Ala | Ala | Ala | Ser | Asp | Thr | Arg | Gly | Leu | Val | Ser | Leu |     |
|     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| TTT | AGC | CCC | GGG | TCG | GCT | CAG | AAA | ATC | CAG | CTC | GTA | AAC | ACC | AAC | GGC | 238 |
| Phe | Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile | Gln | Leu | Val | Asn | Thr | Asn | Gly |     |
| 65  |     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |
| AGT | TGG | CAC | ATC | AAC | AGG | ACT | GCC | CTG | AAC | TGC | AAC | GAC | TCC | CTC | CAA | 286 |
| Ser | Trp | His | Ile | Asn | Arg | Thr | Ala | Leu | Asn | Cys | Asn | Asp | Ser | Leu | Gln |     |
| 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| ACA | GGG | TTC | TTT | GCC | GCA | CTA | TTC | TAC | AAA | CAC | AAA | TTC | AAC | TCG | TCT | 334 |
| Thr | Gly | Phe | Phe | Ala | Ala | Leu | Phe | Tyr | Lys | His | Lys | Phe | Asn | Ser | Ser |     |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| GGA | TGC | CCA | GAG | CGC | TTG | GCC | AGC | TGT | CGC | TCC | ATC | GAC | AAG | TTC | GCT | 382 |
| Gly | Cys | Pro | Glu | Arg | Leu | Ala | Ser | Cys | Arg | Ser | Ile | Asp | Lys | Phe | Ala |     |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| CAG | GGG | TGG | GGT | CCC | CTC | ACT | TAC | ACT | GAG | CCT | AAC | AGC | TCG | GAC | CAG | 430 |
| Gln | Gly | Trp | Gly | Pro | Leu | Thr | Tyr | Thr | Glu | Pro | Asn | Ser | Ser | Asp | Gln |     |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| AGG | CCC | TAC | TGC | TGG | CAC | TAC | GCG | CCT | CGA | CCG | TGT | GGT | ATT | GTA | CCC | 478 |
| Arg | Pro | Tyr | Cys | Trp | His | Tyr | Ala | Pro | Arg | Pro | Cys | Gly | Ile | Val | Pro |     |
|     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |
| GCG | TCT | CAG | GTG | TGC | GGT | CCA | GTG | TAT | TGC | TTC | ACC | CCG | AGC | CCT | GTT | 526 |
| Ala | Ser | Gln | Val | Cys | Gly | Pro | Val | Tyr | Cys | Phe | Thr | Pro | Ser | Pro | Val |     |
| 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| GTG | GTG | GGG | ACG | ACC | GAT | CGG | TTT | GGT | GTG | CCC | ACG | TAT | AAC | TGG | GGG | 574 |
| Val | Val | Gly | Thr | Thr | Asp | Arg | Phe | Gly | Val | Pro | Thr | Tyr | Asn | Trp | Gly |     |
|     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| GCG | AAC | GAC | TCG | GAT | GTG | CTG | ATT | CTC | AAC | AAC | ACG | CGG | CCG | CCG | CGA | 622 |
| Ala | Asn | Asp | Ser | Asp | Val | Leu | Ile | Leu | Asn | Asn | Thr | Arg | Pro | Pro | Arg |     |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG<br>Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys<br>210 215 220     | 670  |
| ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC<br>Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr<br>225 230 235     | 718  |
| TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC<br>Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr<br>240 245 250 255 | 766  |
| GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT<br>Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His<br>260 265 270     | 814  |
| TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC<br>Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile<br>275 280 285     | 862  |
| TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC<br>Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala<br>290 295 300     | 910  |
| GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT<br>Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp<br>305 310 315     | 958  |
| AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GGT GAT CGA GGG<br>Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gly Asp Arg Gly<br>320 325 330 335 | 1006 |
| CAG ACA CCA TCA CCA CCA TCA CTA AT AG<br>Gln Thr Pro Ser Pro Pro Ser Leu<br>340                                                                       | 1034 |

## (2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 343 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Pro | Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ala | Gly | Leu | Ala | Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp | Ala | Lys | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Val | Val | Met | Leu | Leu | Phe | Ala | Gly | Val | Asp | Gly | His | Thr | Arg | Val |
|     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ser | Gly | Gly | Ala | Ala | Ala | Ser | Asp | Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile | Gln | Leu | Val | Asn | Thr | Asn | Gly | Ser |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |

Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr  
                                     85                                    90                                    95  
 Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly  
                                     100                                    105                                    110  
 Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln  
                                     115                                    120                                    125  
 Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg  
                                     130                                    135                                    140  
 Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala  
 145                                    150                                    155                                    160  
 Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val  
                                     165                                    170                                    175  
 Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala  
                                     180                                    185                                    190  
 Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly  
                                     195                                    200                                    205  
 Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr  
                                     210                                    215                                    220  
 Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu  
 225                                    230                                    235                                    240  
 Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala  
                                     245                                    250                                    255  
 Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr  
                                     260                                    265                                    270  
 Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe  
                                     275                                    280                                    285  
 Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala  
                                     290                                    295                                    300  
 Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg  
 305                                    310                                    315                                    320  
 Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gly Asp Arg Gly Gln  
                                     325                                    330                                    335  
 Thr Pro Ser Pro Pro Ser Leu  
                                     340

## (2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 945 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO



(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                  |                   |                   |                   |                   |                  |     |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|------------------|-----|
| ATG<br>Met<br>1   | GTG<br>Val        | GGG<br>Gly        | AAC<br>Asn        | TGG<br>Trp<br>5   | GCT<br>Ala        | AAG<br>Lys        | GTT<br>Val        | TTG<br>Leu        | GTT<br>Val<br>10  | GTG<br>Val       | ATG<br>Met        | CTA<br>Leu        | CTC<br>Leu        | TTT<br>Phe<br>15  | GCC<br>Ala       | 48  |
| GGC<br>Gly        | GTC<br>Val        | GAC<br>Asp<br>20  | GGG<br>Gly        | CAT<br>His        | ACC<br>Thr        | CGC<br>Arg        | GTG<br>Val        | TCA<br>Ser<br>25  | GGA<br>Gly        | GGG<br>Gly       | GCA<br>Ala        | GCA<br>Ala        | GCC<br>Ala<br>30  | TCC<br>Ser        | GAT<br>Asp       | 96  |
| ACC<br>Thr        | AGG<br>Arg        | GGC<br>Gly<br>35  | CTT<br>Leu        | GTG<br>Val        | TCC<br>Ser        | CTC<br>Leu        | TTT<br>Phe<br>40  | AGC<br>Ser        | CCC<br>Pro        | GGG<br>Gly       | TCG<br>Ser        | GCT<br>Ala<br>45  | CAG<br>Gln        | AAA<br>Lys        | ATC<br>Ile       | 144 |
| CAG<br>Gln<br>50  | CTC<br>Leu        | GTA<br>Val        | AAC<br>Asn        | ACC<br>Thr        | AAC<br>Asn        | GGC<br>Gly<br>55  | AGT<br>Ser        | TGG<br>Trp        | CAC<br>His        | ATC<br>Ile       | AAC<br>Asn<br>60  | AGG<br>Arg        | ACT<br>Thr        | GCC<br>Ala        | CTG<br>Leu       | 192 |
| AAC<br>Asn<br>65  | TGC<br>Cys        | AAC<br>Asn        | GAC<br>Asp        | TCC<br>Ser        | CTC<br>Leu<br>70  | CAA<br>Gln        | ACA<br>Thr        | GGG<br>Gly        | TTC<br>Phe        | TTT<br>Phe<br>75 | GCC<br>Ala        | GCA<br>Ala        | CTA<br>Leu        | TTC<br>Phe        | TAC<br>Tyr<br>80 | 240 |
| AAA<br>Lys        | CAC<br>His        | AAA<br>Lys        | TTT<br>Phe        | AAC<br>Asn<br>85  | TCG<br>Ser        | TCT<br>Ser        | GGA<br>Gly        | TGC<br>Cys        | CCA<br>Pro<br>90  | GAG<br>Glu       | CGC<br>Arg        | TTG<br>Leu        | GCC<br>Ala        | AGC<br>Ser<br>95  | TGT<br>Cys       | 288 |
| CGC<br>Arg        | TCC<br>Ser        | ATC<br>Ile        | GAC<br>Asp<br>100 | AAG<br>Lys        | TTC<br>Phe        | GCT<br>Ala        | CAG<br>Gln        | GGG<br>Gly<br>105 | TGG<br>Trp        | GGT<br>Gly       | CCC<br>Pro        | CTC<br>Leu        | ACT<br>Thr<br>110 | TAC<br>Tyr        | ACT<br>Thr       | 336 |
| GAG<br>Glu        | CCT<br>Pro        | AAC<br>Asn<br>115 | AGC<br>Ser        | TCG<br>Ser        | GAC<br>Asp        | CAG<br>Gln        | AGG<br>Arg<br>120 | CCC<br>Pro        | TAC<br>Tyr        | TGC<br>Cys       | TGG<br>Trp        | CAC<br>His<br>125 | TAC<br>Tyr        | GCG<br>Ala        | CCT<br>Pro       | 384 |
| CGA<br>Arg        | CCG<br>Pro<br>130 | TGT<br>Cys        | GGT<br>Gly        | ATT<br>Ile        | GTA<br>Val        | CCC<br>Pro<br>135 | GCG<br>Ala        | TCT<br>Ser        | CAG<br>Gln        | GTG<br>Val       | TGC<br>Cys<br>140 | GGT<br>Gly        | CCA<br>Pro        | GTG<br>Val        | TAT<br>Tyr       | 432 |
| TGC<br>Cys<br>145 | TTC<br>Phe        | ACC<br>Thr        | CCG<br>Pro        | AGC<br>Ser        | CCT<br>Pro<br>150 | GTT<br>Val        | GTG<br>Val        | GTG<br>Val        | GGG<br>Gly<br>155 | ACG<br>Thr       | ACC<br>Thr        | GAT<br>Asp        | CGG<br>Arg        | TTT<br>Phe<br>160 | GGT<br>Gly       | 480 |
| GTC<br>Val        | CCC<br>Pro        | ACG<br>Thr        | TAT<br>Tyr        | AAC<br>Asn<br>165 | TGG<br>Trp        | GGG<br>Gly        | GCG<br>Ala        | AAC<br>Asn        | GAC<br>Asp<br>170 | TCG<br>Ser       | GAT<br>Asp        | GTG<br>Val        | CTG<br>Leu        | ATT<br>Ile<br>175 | CTC<br>Leu       | 528 |
| AAC<br>Asn        | AAC<br>Asn        | ACG<br>Thr        | CGG<br>Arg<br>180 | CCG<br>Pro        | CCG<br>Pro        | CGA<br>Arg        | GGC<br>Gly        | AAC<br>Asn<br>185 | TGG<br>Trp        | TTC<br>Phe       | GGC<br>Gly        | TGT<br>Cys        | ACA<br>Thr<br>190 | TGG<br>Trp        | ATG<br>Met       | 576 |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC | 624 |
| Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile |     |
| 195 200 205                                                     |     |
| GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG | 672 |
| Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg |     |
| 210 215 220                                                     |     |
| AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG | 720 |
| Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu |     |
| 225 230 235 240                                                 |     |
| ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC | 768 |
| Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro |     |
| 245 250 255                                                     |     |
| TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC | 816 |
| Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly |     |
| 260 265 270                                                     |     |
| GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT | 864 |
| Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg |     |
| 275 280 285                                                     |     |
| TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG | 912 |
| Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu |     |
| 290 295 300                                                     |     |
| TCT ACA ACA GAG TGG CAG AGC TTA ATT AAT TAG                     | 945 |
| Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn                         |     |
| 305 310                                                         |     |

## (2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala |  |
| 1 5 10 15                                                       |  |
| Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp |  |
| 20 25 30                                                        |  |
| Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile |  |
| 35 40 45                                                        |  |
| Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu |  |
| 50 55 60                                                        |  |
| Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr |  |
| 65 70 75 80                                                     |  |
| Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys |  |
| 85 90 95                                                        |  |

Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr  
 100 105 110  
 Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro  
 115 120 125  
 Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr  
 130 135 140  
 Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly  
 145 150 155 160  
 Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu  
 165 170 175  
 Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met  
 180 185 190  
 Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile  
 195 200 205  
 Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg  
 210 215 220  
 Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu  
 225 230 235 240  
 Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro  
 245 250 255  
 Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly  
 260 265 270  
 Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg  
 275 280 285  
 Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu  
 290 295 300  
 Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn  
 305 310

## (2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 961 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..958

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

|                   |                   |                  |                   |                   |                   |                   |                   |                   |                   |                  |                   |                   |                   |                   |            |     |
|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|------------|-----|
| ATG<br>Met<br>1   | GTG<br>Val        | GGG<br>Gly       | AAC<br>Asn        | TGG<br>Trp<br>5   | GCT<br>Ala        | AAG<br>Lys        | GTT<br>Val        | TTG<br>Leu        | GTT<br>Val<br>10  | GTG<br>Val       | ATG<br>Met        | CTA<br>Leu        | CTC<br>Leu        | TTT<br>Phe<br>15  | GCC<br>Ala | 48  |
| GGC<br>Gly        | GTC<br>Val        | GAC<br>Asp       | GGG<br>Gly<br>20  | CAT<br>His        | ACC<br>Thr        | CGC<br>Arg        | GTT<br>Val<br>25  | TCA<br>Ser        | GGA<br>Gly        | GGG<br>Gly       | GCA<br>Ala        | GCA<br>Ala        | GCC<br>Ala<br>30  | TCC<br>Ser        | GAT<br>Asp | 96  |
| ACC<br>Thr        | AGG<br>Arg        | GGC<br>Gly<br>35 | CTT<br>Leu        | GTG<br>Val        | TCC<br>Ser        | CTC<br>Leu        | TTT<br>Phe<br>40  | AGC<br>Ser        | CCC<br>Pro        | GGG<br>Gly       | TCG<br>Ser        | GCT<br>Ala<br>45  | CAG<br>Gln        | AAA<br>Lys        | ATC<br>Ile | 144 |
| CAG<br>Gln<br>50  | CTC<br>Leu        | GTA<br>Val       | AAC<br>Asn        | ACC<br>Thr        | AAC<br>Asn        | GGC<br>Gly<br>55  | AGT<br>Ser        | TGG<br>Trp        | CAC<br>His        | ATC<br>Ile       | AAC<br>Asn<br>60  | AGG<br>Arg        | ACT<br>Thr        | GCC<br>Ala        | CTG<br>Leu | 192 |
| AAC<br>Asn<br>65  | TGC<br>Cys        | AAC<br>Asn       | GAC<br>Asp        | TCC<br>Ser        | CTC<br>Leu<br>70  | CAA<br>Gln        | ACA<br>Thr        | GGG<br>Gly        | TTC<br>Phe        | TTT<br>Phe<br>75 | GCC<br>Ala        | GCA<br>Ala        | CTA<br>Leu        | TTC<br>Phe<br>80  | TAC<br>Tyr | 240 |
| AAA<br>Lys        | CAC<br>His        | AAA<br>Lys       | TTC<br>Phe<br>85  | AAC<br>Asn        | TCG<br>Ser        | TCT<br>Ser        | GGA<br>Gly        | TGC<br>Cys        | CCA<br>Pro<br>90  | GAG<br>Glu       | CGC<br>Arg        | TTG<br>Leu        | GCC<br>Ala<br>95  | AGC<br>Ser        | TGT<br>Cys | 288 |
| CGC<br>Arg        | TCC<br>Ser        | ATC<br>Ile       | GAC<br>Asp<br>100 | AAG<br>Lys        | TTC<br>Phe        | GCT<br>Ala        | CAG<br>Gln        | GGG<br>Gly<br>105 | TGG<br>Trp        | GGT<br>Gly       | CCC<br>Pro        | CTC<br>Leu        | ACT<br>Thr<br>110 | TAC<br>Tyr        | ACT<br>Thr | 336 |
| GAG<br>Glu        | CCT<br>Pro<br>115 | AAC<br>Asn       | AGC<br>Ser        | TCG<br>Ser        | GAC<br>Asp        | CAG<br>Gln        | AGG<br>Arg<br>120 | CCC<br>Pro        | TAC<br>Tyr        | TGC<br>Cys       | TGG<br>Trp        | CAC<br>His<br>125 | TAC<br>Tyr        | GCG<br>Ala        | CCT<br>Pro | 384 |
| CGA<br>Arg<br>130 | CCG<br>Pro        | TGT<br>Cys       | GGT<br>Gly        | ATT<br>Ile        | GTA<br>Val        | CCC<br>Pro<br>135 | GCG<br>Ala        | TCT<br>Ser        | CAG<br>Gln        | GTG<br>Val       | TGC<br>Cys<br>140 | GGT<br>Gly        | CCA<br>Pro        | GTG<br>Val        | TAT<br>Tyr | 432 |
| TGC<br>Cys<br>145 | TTC<br>Phe        | ACC<br>Thr       | CCG<br>Pro        | AGC<br>Ser        | CCT<br>Pro<br>150 | GTT<br>Val        | GTG<br>Val        | GTG<br>Val        | GGG<br>Gly<br>155 | ACG<br>Thr       | ACC<br>Thr        | GAT<br>Asp        | CGG<br>Arg        | TTT<br>Phe<br>160 | GGT<br>Gly | 480 |
| GTC<br>Val        | CCC<br>Pro        | ACG<br>Thr       | TAT<br>Tyr        | AAC<br>Asn<br>165 | TGG<br>Trp        | GGG<br>Gly        | GCG<br>Ala        | AAC<br>Asn        | GAC<br>Asp<br>170 | TCG<br>Ser       | GAT<br>Asp        | GTG<br>Val        | CTG<br>Leu        | ATT<br>Ile<br>175 | CTC<br>Leu | 528 |
| AAC<br>Asn        | AAC<br>Asn        | ACG<br>Thr       | CGG<br>Arg<br>180 | CCG<br>Pro        | CCG<br>Pro        | CGA<br>Arg        | GGC<br>Gly        | AAC<br>Asn<br>185 | TGG<br>Trp        | TTC<br>Phe       | GGC<br>Gly        | TGT<br>Cys        | ACA<br>Thr<br>190 | TGG<br>Trp        | ATG<br>Met | 576 |
| AAT<br>Asn        | GGC<br>Gly<br>195 | ACT<br>Thr       | GGG<br>Gly        | TTC<br>Phe        | ACC<br>Thr        | AAG<br>Lys        | ACG<br>Thr<br>200 | TGT<br>Cys        | GGG<br>Gly        | GGC<br>Gly       | CCC<br>Pro        | CCG<br>Pro<br>205 | TGC<br>Cys        | AAC<br>Asn        | ATC<br>Ile | 624 |
| GGG<br>Gly<br>210 | GGG<br>Gly        | GCC<br>Ala       | GGC<br>Gly        | AAC<br>Asn        | AAC<br>Asn        | ACC<br>Thr<br>215 | TTG<br>Leu        | ACC<br>Thr        | TGC<br>Cys        | CCC<br>Pro       | ACT<br>Thr<br>220 | GAC<br>Asp        | TGT<br>Cys        | TTT<br>Phe        | CGG<br>Arg | 672 |
| AAG<br>Met        | CAC<br>His        | CCC<br>Pro       | GAG<br>Glu        | GCC<br>Ala        | ACC<br>Thr        | TAC<br>Tyr        | GCC<br>Ala        | AGA<br>Ser        | TGC<br>Cys        | GGT<br>Gly       | TCT<br>Ser        | GGG<br>Gly        | CCC<br>Pro        | TGG<br>Trp        | CTG<br>Leu | 720 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | His | Pro | Glu | Ala | Thr | Tyr | Ala | Arg | Cys | Gly | Ser | Gly | Pro | Trp | Leu |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| ACA | CCT | AGG | TGT | ATG | GTT | CAT | TAC | CCA | TAT | AGG | CTC | TGG | CAC | TAC | CCC | 768 |
| Thr | Pro | Arg | Cys | Met | Val | His | Tyr | Pro | Tyr | Arg | Leu | Trp | His | Tyr | Pro |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| TGC | ACT | GTC | AAC | TTC | ACC | ATC | TTC | AAG | GTT | AGG | ATG | TAC | GTG | GGG | GGC | 816 |
| Cys | Thr | Val | Asn | Phe | Thr | Ile | Phe | Lys | Val | Arg | Met | Tyr | Val | Gly | Gly |     |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| GTG | GAG | CAC | AGG | TTC | GAA | GCC | GCA | TGC | AAT | TGG | ACT | CGA | GGA | GAG | CGT | 864 |
| Val | Glu | His | Arg | Phe | Glu | Ala | Ala | Cys | Asn | Trp | Thr | Arg | Gly | Glu | Arg |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| TGT | GAC | TTG | GAG | GAC | AGG | GAT | AGA | TCA | GAG | CTT | AGC | CCG | CTG | CTG | CTG | 912 |
| Cys | Asp | Leu | Glu | Asp | Arg | Asp | Arg | Ser | Glu | Leu | Ser | Pro | Leu | Leu | Leu |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| TCT | ACA | ACA | GGT | GAT | CGA | GGG | CAG | ACA | CCA | TCA | CCA | CCA | TCA | CTA | A   | 958 |
| Ser | Thr | Thr | Gly | Asp | Arg | Gly | Gln | Thr | Pro | Ser | Pro | Pro | Ser | Leu |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     |     |
| TAG |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 961 |

## (2) INFORMATION FOR SEQ ID NO: 44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Val | Gly | Asn | Trp | Ala | Lys | Val | Leu | Val | Val | Met | Leu | Leu | Phe | Ala |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Gly | Val | Asp | Gly | His | Thr | Arg | Val | Ser | Gly | Gly | Ala | Ala | Ala | Ser | Asp |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe | Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Gln | Leu | Val | Asn | Thr | Asn | Gly | Ser | Trp | His | Ile | Asn | Arg | Thr | Ala | Leu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Asn | Cys | Asn | Asp | Ser | Leu | Gln | Thr | Gly | Phe | Phe | Ala | Ala | Leu | Phe | Tyr |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Lys | His | Lys | Phe | Asn | Ser | Ser | Gly | Cys | Pro | Glu | Arg | Leu | Ala | Ser | Cys |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Arg | Ser | Ile | Asp | Lys | Phe | Ala | Gln | Gly | Trp | Gly | Pro | Leu | Thr | Tyr | Thr |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Glu | Pro | Asn | Ser | Ser | Asp | Gln | Arg | Pro | Tyr | Cys | Trp | His | Tyr | Ala | Pro |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Arg | Pro | Cys | Gly | Ile | Val | Pro | Ala | Ser | Gln | Val | Cys | Gly | Pro | Val | Tyr |  |

| 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Phe | Thr | Pro | Ser | Pro | Val | Val | Val | Gly | Thr | Thr | Asp | Arg | Phe | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Pro | Thr | Tyr | Asn | Trp | Gly | Ala | Asn | Asp | Ser | Asp | Val | Leu | Ile | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asn | Asn | Thr | Arg | Pro | Pro | Arg | Gly | Asn | Trp | Phe | Gly | Cys | Thr | Trp | Met |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asn | Gly | Thr | Gly | Phe | Thr | Lys | Thr | Cys | Gly | Gly | Pro | Pro | Cys | Asn | Ile |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Gly | Ala | Gly | Asn | Asn | Thr | Leu | Thr | Cys | Pro | Thr | Asp | Cys | Phe | Arg |
|     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Lys | His | Pro | Glu | Ala | Thr | Tyr | Ala | Arg | Cys | Gly | Ser | Gly | Pro | Trp | Leu |
| 225 |     |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Thr | Pro | Arg | Cys | Met | Val | His | Tyr | Pro | Tyr | Arg | Leu | Trp | His | Tyr | Pro |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Cys | Thr | Val | Asn | Phe | Thr | Ile | Phe | Lys | Val | Arg | Met | Tyr | Val | Gly | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Glu | His | Arg | Phe | Glu | Ala | Ala | Cys | Asn | Trp | Thr | Arg | Gly | Glu | Arg |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Cys | Asp | Leu | Glu | Asp | Arg | Asp | Arg | Ser | Glu | Leu | Ser | Pro | Leu | Leu | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ser | Thr | Thr | Gly | Asp | Arg | Gly | Gln | Thr | Pro | Ser | Pro | Pro | Ser | Leu |     |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1395 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1392

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..1389

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC TAC TAT

| Met<br>1          | Val              | Ala               | Gly               | Ala<br>5          | His               | Trp               | Gly               | Val               | Leu<br>10         | Ala               | Gly               | Leu               | Ala               | Tyr<br>15         | Tyr               |     |
|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| TCC<br>Ser        | ATG<br>Met       | GTG<br>Val        | GGG<br>Gly<br>20  | AAC<br>Asn        | TGG<br>Trp        | GCT<br>Ala        | AAG<br>Lys        | GTT<br>Val<br>25  | TTG<br>Leu        | GTT<br>Val        | GTG<br>Val        | ATG<br>Met        | CTA<br>Leu<br>30  | CTC<br>Leu        | TTT<br>Phe        | 96  |
| GCC<br>Ala        | GGC<br>Gly       | GTC<br>Val<br>35  | GAC<br>Asp        | GGG<br>Gly        | CAT<br>His        | ACC<br>Thr        | CGC<br>Arg<br>40  | GTG<br>Val        | TCA<br>Ser        | GGA<br>Gly        | GGG<br>Gly        | GCA<br>Ala<br>45  | GCA<br>Ala        | GCC<br>Ala        | TCC<br>Ser        | 144 |
| GAT<br>Asp        | ACC<br>Thr<br>50 | AGG<br>Arg        | GGC<br>Gly        | CTT<br>Leu        | GTG<br>Val        | TCC<br>Ser<br>55  | CTC<br>Leu        | TTT<br>Phe        | AGC<br>Ser        | CCC<br>Pro        | GGG<br>Gly<br>60  | TCG<br>Ser        | GCT<br>Ala        | CAG<br>Gln        | AAA<br>Lys        | 192 |
| ATC<br>Ile<br>65  | CAG<br>Gln       | CTC<br>Leu        | GTA<br>Val        | AAC<br>Asn        | ACC<br>Thr<br>70  | AAC<br>Asn        | GGC<br>Gly        | AGT<br>Ser        | TGG<br>Trp        | CAC<br>His<br>75  | ATC<br>Ile        | AAC<br>Asn        | AGG<br>Arg        | ACT<br>Thr        | GCC<br>Ala<br>80  | 240 |
| CTG<br>Leu        | AAC<br>Asn       | TGC<br>Cys        | AAC<br>Asn        | GAC<br>Asp<br>85  | TCC<br>Ser        | CTC<br>Leu        | CAA<br>Gln        | ACA<br>Thr        | GGG<br>Gly<br>90  | TTC<br>Phe        | TTT<br>Phe        | GCC<br>Ala        | GCA<br>Ala        | CTA<br>Leu<br>95  | TTC<br>Phe        | 288 |
| TAC<br>Tyr        | AAA<br>Lys       | CAC<br>His        | AAA<br>Lys<br>100 | TTC<br>Phe        | AAC<br>Asn        | TCG<br>Ser        | TCT<br>Ser        | GGA<br>Gly<br>105 | TGC<br>Cys        | CCA<br>Pro        | GAG<br>Glu        | CGC<br>Arg        | TTG<br>Leu<br>110 | GCC<br>Ala        | AGC<br>Ser        | 336 |
| TGT<br>Cys        | CGC<br>Arg       | TCC<br>Ser<br>115 | ATC<br>Ile        | GAC<br>Asp        | AAG<br>Lys        | TTC<br>Phe        | GCT<br>Ala<br>120 | CAG<br>Gln        | GGG<br>Gly        | TGG<br>Trp        | GGT<br>Gly        | CCC<br>Pro<br>125 | CTC<br>Leu        | ACT<br>Thr        | TAC<br>Tyr        | 384 |
| ACT<br>Thr<br>130 | GAG<br>Glu       | CCT<br>Pro        | AAC<br>Asn        | AGC<br>Ser        | TCG<br>Ser        | GAC<br>Asp<br>135 | CAG<br>Gln        | AGG<br>Arg        | CCC<br>Pro        | TAC<br>Tyr        | TGC<br>Cys<br>140 | TGG<br>Trp        | CAC<br>His        | TAC<br>Tyr        | GCG<br>Ala        | 432 |
| CCT<br>Pro<br>145 | CGA<br>Arg       | CCG<br>Pro        | TGT<br>Cys        | GGT<br>Gly        | ATT<br>Ile<br>150 | GTA<br>Val        | CCC<br>Pro        | GCG<br>Ala        | TCT<br>Ser        | CAG<br>Gln<br>155 | GTG<br>Val        | TGC<br>Cys        | GGT<br>Gly        | CCA<br>Pro        | GTG<br>Val<br>160 | 480 |
| TAT<br>Tyr        | TGC<br>Cys       | TTC<br>Phe        | ACC<br>Thr        | CCG<br>Pro<br>165 | AGC<br>Ser        | CCT<br>Pro        | GTT<br>Val        | GTG<br>Val        | GTG<br>Val<br>170 | GGG<br>Gly        | ACG<br>Thr        | ACC<br>Thr        | GAT<br>Asp        | CGG<br>Arg<br>175 | TTT<br>Phe        | 528 |
| GGT<br>Gly        | GTC<br>Val       | CCC<br>Pro        | ACG<br>Thr<br>180 | TAT<br>Tyr        | AAC<br>Asn        | TGG<br>Trp        | GGG<br>Gly        | GCG<br>Ala<br>185 | AAC<br>Asn        | GAC<br>Asp        | TCG<br>Ser        | GAT<br>Asp        | GTG<br>Val<br>190 | CTG<br>Leu        | ATT<br>Ile        | 576 |
| CTC<br>Leu        | AAC<br>Asn       | AAC<br>Asn<br>195 | ACG<br>Thr        | CGG<br>Arg        | CCG<br>Pro        | CCG<br>Pro        | CGA<br>Arg<br>200 | GGC<br>Gly        | AAC<br>Asn        | TGG<br>Trp        | TTC<br>Phe        | GGC<br>Gly<br>205 | TGT<br>Cys        | ACA<br>Thr        | TGG<br>Trp        | 624 |
| ATG<br>Met<br>210 | AAT<br>Asn       | GGC<br>Gly        | ACT<br>Thr        | GGG<br>Gly        | TTC<br>Phe        | ACC<br>Thr<br>215 | AAG<br>Lys        | ACG<br>Thr        | TGT<br>Cys        | GGG<br>Gly        | GGC<br>Gly<br>220 | CCC<br>Pro        | CCG<br>Pro        | TGC<br>Cys        | AAC<br>Asn        | 672 |
| ATC<br>Ile<br>225 | GGG<br>Gly       | GGG<br>Gly        | GCC<br>Ala        | GGC<br>Gly        | AAC<br>Asn<br>230 | AAC<br>Asn        | ACC<br>Thr        | TTG<br>Leu        | ACC<br>Thr        | TGC<br>Cys<br>235 | CCC<br>Pro        | ACT<br>Thr        | GAC<br>Asp        | TGT<br>Cys        | TTT<br>Phe<br>240 | 720 |
| CGG<br>Arg        | AAG<br>Lys       | CAC<br>His        | CCC<br>Pro        | GAG<br>Glu<br>245 | GCC<br>Ala        | ACC<br>Thr        | TAC<br>Tyr        | GCC<br>Ala        | AGA<br>Arg<br>250 | TGC<br>Cys        | GGT<br>Gly        | TCT<br>Ser        | GGG<br>Gly        | CCC<br>Pro<br>255 | TGG<br>Trp        | 768 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |        |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--------|------|
| CTG | ACA | CCT | AGG | TGT | ATG | GTT | CAT | TAC | CCA | TAT | AGG | CTC | TGG | CAC | TAC    | 816  |
| Leu | Thr | Pro | Arg | Cys | Met | Val | His | Tyr | Pro | Tyr | Arg | Leu | Trp | His | Tyr    |      |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |        |      |
| CCC | TGC | ACT | GTC | AAC | TTC | ACC | ATC | TTC | AAG | GTT | AGG | ATG | TAC | GTG | GGG    | 864  |
| Pro | Cys | Thr | Val | Asn | Phe | Thr | Ile | Phe | Lys | Val | Arg | Met | Tyr | Val | Gly    |      |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |        |      |
| GGC | GTG | GAG | CAC | AGG | TTC | GAA | GCC | GCA | TGC | AAT | TGG | ACT | CGA | GGA | GAG    | 912  |
| Gly | Val | Glu | His | Arg | Phe | Glu | Ala | Ala | Cys | Asn | Trp | Thr | Arg | Gly | Glu    |      |
|     |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |        |      |
| CGT | TGT | GAC | TTG | GAG | GAC | AGG | GAT | AGA | TCA | GAG | CTT | AGC | CCG | CTG | CTG    | 960  |
| Arg | Cys | Asp | Leu | Glu | Asp | Arg | Asp | Arg | Ser | Glu | Leu | Ser | Pro | Leu | Leu    |      |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320    |      |
| CTG | TCT | ACA | ACA | GAG | TGG | CAG | ATA | CTG | CCC | TGT | TCC | TTC | ACC | ACC | CTG    | 1008 |
| Leu | Ser | Thr | Thr | Glu | Trp | Gln | Ile | Leu | Pro | Cys | Ser | Phe | Thr | Thr | Leu    |      |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |        |      |
| CCG | GCC | CTA | TCC | ACC | GGC | CTG | ATC | CAC | CTC | CAT | CAG | AAC | ATC | GTG | GAC    | 1056 |
| Pro | Ala | Leu | Ser | Thr | Gly | Leu | Ile | His | Leu | His | Gln | Asn | Ile | Val | Asp    |      |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |        |      |
| GTG | CAA | TAC | CTG | TAC | GGT | GTA | GGG | TGG | GCG | GTT | GTC | TCC | CTT | GTC | ATC    | 1104 |
| Val | Gln | Tyr | Leu | Tyr | Gly | Val | Gly | Ser | Ala | Val | Val | Ser | Leu | Val | Ile    |      |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |        |      |
| AAA | TGG | GAG | TAT | GTC | CTG | TTG | CTC | TTC | CTT | CTC | CTG | GCA | GAC | GCG | CGC    | 1152 |
| Lys | Trp | Glu | Tyr | Val | Leu | Leu | Leu | Phe | Leu | Leu | Leu | Ala | Asp | Ala | Arg    |      |
|     |     |     | 370 |     |     |     | 375 |     |     |     | 380 |     |     |     |        |      |
| ATC | TGC | GCC | TGC | TTA | TGG | ATG | ATG | CTG | CTG | ATA | GCT | CAA | GCT | GAG | GCC    | 1200 |
| Ile | Cys | Ala | Cys | Leu | Trp | Met | Met | Leu | Leu | Ile | Ala | Gln | Ala | Glu | Ala    |      |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400    |      |
| GCC | TTA | GAG | AAC | CTG | GTG | GTC | CTC | AAT | GCG | GCG | GCC | GTG | GCC | GGG | GCG    | 1248 |
| Ala | Leu | Glu | Asn | Leu | Val | Val | Leu | Asn | Ala | Ala | Ala | Val | Ala | Gly | Ala    |      |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     | 415 |     |        |      |
| CAT | GGC | ACT | CTT | TCC | TTC | CTT | GTG | TTC | TTC | TGT | GCT | GCC | TGG | TAC | ATC    | 1296 |
| His | Gly | Thr | Leu | Ser | Phe | Leu | Val | Phe | Phe | Cys | Ala | Ala | Trp | Tyr | Ile    |      |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |        |      |
| AAG | GGC | AGG | CTG | GTC | CCT | GGT | GCG | GCA | TAC | GCC | TTC | TAT | GGC | GTG | TGG    | 1344 |
| Lys | Gly | Arg | Leu | Val | Pro | Gly | Ala | Ala | Tyr | Ala | Phe | Tyr | Gly | Val | Trp    |      |
|     |     |     | 435 |     |     |     | 440 |     |     |     |     | 445 |     |     |        |      |
| CCG | CTG | CTC | CTG | CTT | CTG | CTG | GCC | TTA | CCA | CCA | CGA | GCT | TAT | GCC | TAGTAA | 1395 |
| Pro | Leu | Leu | Leu | Leu | Leu | Leu | Ala | Leu | Pro | Pro | Arg | Ala | Tyr | Ala |        |      |
|     |     |     | 450 |     |     |     | 455 |     |     |     | 460 |     |     |     |        |      |

## (2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 463 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein



|            |           |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|-----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Val       | Ala        | Gly        | Ala<br>5   | His        | Trp        | Gly        | Val        | Leu<br>10  | Ala        | Gly        | Leu        | Ala        | Tyr<br>15  | Tyr        |
| Ser        | Met       | Val        | Gly<br>20  | Asn        | Trp        | Ala        | Lys        | Val<br>25  | Leu        | Val        | Val        | Met        | Leu<br>30  | Leu        | Phe        |
| Ala        | Gly       | Val<br>35  | Asp        | Gly        | His        | Thr        | Arg<br>40  | Val        | Ser        | Gly        | Gly        | Ala<br>45  | Ala        | Ala        | Ser        |
| Asp        | Thr<br>50 | Arg        | Gly        | Leu        | Val        | Ser<br>55  | Leu        | Phe        | Ser        | Pro        | Gly<br>60  | Ser        | Ala        | Gln        | Lys        |
| Ile<br>65  | Gln       | Leu        | Val        | Asn<br>70  | Thr        | Asn        | Gly        | Ser        | Trp        | His<br>75  | Ile        | Asn        | Arg        | Thr        | Ala<br>80  |
| Leu        | Asn       | Cys        | Asn        | Asp<br>85  | Ser        | Leu        | Gln        | Thr        | Gly<br>90  | Phe        | Phe        | Ala        | Ala        | Leu<br>95  | Phe        |
| Tyr        | Lys       | His<br>100 | Lys        | Phe        | Asn        | Ser        | Ser        | Gly<br>105 | Cys        | Pro        | Glu        | Arg        | Leu<br>110 | Ala        | Ser        |
| Cys        | Arg       | Ser<br>115 | Ile        | Asp        | Lys        | Phe        | Ala<br>120 | Gln        | Gly        | Trp        | Gly        | Pro<br>125 | Leu        | Thr        | Tyr        |
| Thr<br>130 | Glu       | Pro        | Asn        | Ser        | Ser        | Asp<br>135 | Gln        | Arg        | Pro        | Tyr        | Cys<br>140 | Trp        | His        | Tyr        | Ala        |
| Pro<br>145 | Arg       | Pro        | Cys        | Gly        | Ile<br>150 | Val        | Pro        | Ala        | Ser        | Gln<br>155 | Val        | Cys        | Gly        | Pro        | Val<br>160 |
| Tyr        | Cys       | Phe        | Thr        | Pro<br>165 | Ser        | Pro        | Val        | Val        | Val<br>170 | Gly        | Thr        | Thr        | Asp        | Arg<br>175 | Phe        |
| Gly        | Val       | Pro        | Thr<br>180 | Tyr        | Asn        | Trp        | Gly        | Ala<br>185 | Asn        | Asp        | Ser        | Asp        | Val<br>190 | Leu        | Ile        |
| Leu        | Asn       | Asn<br>195 | Thr        | Arg        | Pro        | Pro        | Arg<br>200 | Gly        | Asn        | Trp        | Phe        | Gly<br>205 | Cys        | Thr        | Trp        |
| Met<br>210 | Asn       | Gly        | Thr        | Gly        | Phe        | Thr<br>215 | Lys        | Thr        | Cys        | Gly        | Gly<br>220 | Pro        | Pro        | Cys        | Asn        |
| Ile<br>225 | Gly       | Gly        | Ala        | Gly        | Asn<br>230 | Asn        | Thr        | Leu        | Thr        | Cys<br>235 | Pro        | Thr        | Asp        | Cys        | Phe<br>240 |
| Arg        | Lys       | His        | Pro        | Glu<br>245 | Ala        | Thr        | Tyr        | Ala<br>250 | Arg        | Cys        | Gly        | Ser        | Gly        | Pro<br>255 | Trp        |
| Leu        | Thr       | Pro        | Arg<br>260 | Cys        | Met        | Val        | His        | Tyr<br>265 | Pro        | Tyr        | Arg        | Leu        | Trp<br>270 | His        | Tyr        |
| Pro        | Cys       | Thr<br>275 | Val        | Asn        | Phe        | Thr        | Ile<br>280 | Phe        | Lys        | Val        | Arg        | Met<br>285 | Tyr        | Val        | Gly        |
| Gly<br>290 | Val       | Glu        | His        | Arg        | Phe        | Glu<br>295 | Ala        | Ala        | Cys        | Asn        | Trp<br>300 | Thr        | Arg        | Gly        | Glu        |
| Arg<br>305 | Cys       | Asp        | Leu        | Glu<br>310 | Asp        | Arg        | Asp        | Arg        | Ser        | Glu<br>315 | Leu        | Ser        | Pro        | Leu        | Leu<br>320 |

Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu  
 325 330 335  
 Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp  
 340 345 350  
 Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile  
 355 360 365  
 Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg  
 370 375 380  
 Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala  
 385 390 395 400  
 Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala  
 405 410 415  
 His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile  
 420 425 430  
 Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp  
 435 440 445  
 Pro Leu Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala  
 450 455 460

## (2) INFORMATION FOR SEQ ID NO: 47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2079

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..2076

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC  
 Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu  
 1 5 10 15  
 GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG  
 Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg  
 20 25 30

48

96

|                   |                   |                   |            |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |     |
|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| GCC<br>Ala        | CTG<br>Leu        | GCG<br>Ala<br>35  | CAT<br>His | GGC<br>Gly        | GTC<br>Val        | CGG<br>Arg        | GTT<br>Val<br>40  | CTG<br>Leu        | GAG<br>Glu        | GAC<br>Asp        | GGC<br>Gly        | GTG<br>Val<br>45  | AAC<br>Asn        | TAT<br>Tyr        | GCA<br>Ala        | 144 |
| ACA<br>Thr        | GGG<br>Gly<br>50  | AAT<br>Asn        | TTG<br>Leu | CCC<br>Pro        | GGT<br>Gly        | TGC<br>Cys<br>55  | TCT<br>Ser        | TTC<br>Phe        | TCT<br>Ser        | ATC<br>Ile        | TTC<br>Phe<br>60  | CTC<br>Leu        | TTG<br>Leu        | GCT<br>Ala        | TTG<br>Leu        | 192 |
| CTG<br>Leu<br>65  | TCC<br>Ser        | TGT<br>Cys        | CTG<br>Leu | ACC<br>Thr        | GTT<br>Val<br>70  | CCA<br>Pro        | GCT<br>Ala        | TCC<br>Ser        | GCT<br>Ala        | TAT<br>Tyr<br>75  | GAA<br>Glu        | GTG<br>Val        | CGC<br>Arg        | AAC<br>Asn        | GTG<br>Val<br>80  | 240 |
| TCC<br>Ser        | GGG<br>Gly        | ATG<br>Met        | TAC<br>Tyr | CAT<br>His<br>85  | GTC<br>Val        | ACG<br>Thr        | AAC<br>Asn        | GAC<br>Asp        | TGC<br>Cys<br>90  | TCC<br>Ser        | AAC<br>Asn        | TCA<br>Ser        | AGC<br>Ser        | ATT<br>Ile<br>95  | GTG<br>Val        | 288 |
| TAT<br>Tyr        | GAG<br>Glu        | GCA<br>Ala<br>100 | GCG<br>Ala | GAC<br>Asp        | ATG<br>Met        | ATC<br>Ile        | ATG<br>Met<br>105 | CAC<br>His        | ACC<br>Thr        | CCC<br>Pro        | GGG<br>Gly        | TGC<br>Cys<br>110 | GTG<br>Val<br>110 | CCC<br>Pro        | TGC<br>Cys        | 336 |
| GTT<br>Val        | CGG<br>Arg<br>115 | GAG<br>Glu        | AAC<br>Asn | AAC<br>Asn        | TCT<br>Ser        | TCC<br>Ser        | CGC<br>Arg<br>120 | TGC<br>Cys        | TGG<br>Trp        | GTA<br>Val        | GCG<br>Ala        | CTC<br>Leu<br>125 | ACC<br>Thr        | CCC<br>Pro        | ACG<br>Thr        | 384 |
| CTC<br>Leu<br>130 | GCA<br>Ala        | GCT<br>Ala        | AGG<br>Arg | AAC<br>Asn        | GCC<br>Ala        | AGC<br>Ser<br>135 | GTC<br>Val        | CCC<br>Pro        | ACC<br>Thr        | ACG<br>Thr        | ACA<br>Thr<br>140 | ATA<br>Ile        | CGA<br>Arg        | CGC<br>Arg        | CAC<br>His        | 432 |
| GTC<br>Val<br>145 | GAT<br>Asp        | TTG<br>Leu        | CTC<br>Leu | GTT<br>Val        | GGG<br>Gly<br>150 | GCG<br>Ala        | GCT<br>Ala        | GCT<br>Ala        | TTC<br>Phe        | TGT<br>Cys<br>155 | TCC<br>Ser        | GCT<br>Ala        | ATG<br>Met        | TAC<br>Tyr        | GTG<br>Val<br>160 | 480 |
| GGG<br>Gly        | GAC<br>Asp        | CTC<br>Leu        | TGC<br>Cys | GGA<br>Gly<br>165 | TCT<br>Ser        | GTC<br>Val        | TTC<br>Phe        | CTC<br>Leu        | GTC<br>Val<br>170 | TCC<br>Ser        | CAG<br>Gln        | CTG<br>Leu        | TTC<br>Phe        | ACC<br>Thr<br>175 | ATC<br>Ile        | 528 |
| TCG<br>Ser        | CCT<br>Pro        | CGC<br>Arg<br>180 | CGG<br>Arg | CAT<br>His        | GAG<br>Glu        | ACG<br>Thr        | GTG<br>Val<br>185 | CAG<br>Gln        | GAC<br>Asp        | TGC<br>Cys        | AAT<br>Asn        | TGC<br>Cys        | TCA<br>Ser<br>190 | ATC<br>Ile        | TAT<br>Tyr        | 576 |
| CCC<br>Pro        | GGC<br>Gly<br>195 | CAC<br>His        | ATA<br>Ile | ACG<br>Thr        | GGT<br>Gly        | CAC<br>His<br>200 | CGT<br>Arg        | ATG<br>Met        | GCT<br>Ala        | TGG<br>Trp        | GAT<br>Asp<br>205 | ATG<br>Met<br>205 | ATG<br>Met        | ATG<br>Met        | AAC<br>Asn        | 624 |
| TGG<br>Trp<br>210 | TCG<br>Ser        | CCT<br>Pro        | ACA<br>Thr | ACG<br>Thr        | GCC<br>Ala        | CTG<br>Leu<br>215 | GTG<br>Val        | GTA<br>Val        | TCG<br>Ser        | CAG<br>Gln        | CTG<br>Leu<br>220 | CTC<br>Leu        | CGG<br>Arg        | ATC<br>Ile        | CCA<br>Pro        | 672 |
| CAA<br>Gln<br>225 | GCT<br>Ala        | GTC<br>Val        | GTG<br>Val | GAC<br>Asp        | ATG<br>Met<br>230 | GTG<br>Val        | GCG<br>Ala        | GGG<br>Gly        | GCC<br>Ala        | CAT<br>His<br>235 | TGG<br>Trp        | GGA<br>Gly        | GTC<br>Val        | CTG<br>Leu        | GCG<br>Ala<br>240 | 720 |
| GGC<br>Gly        | CTC<br>Leu        | GCC<br>Ala        | TAC<br>Tyr | TAT<br>Tyr<br>245 | TCC<br>Ser        | ATG<br>Met        | GTG<br>Val        | GGG<br>Gly<br>250 | AAC<br>Asn<br>250 | TGG<br>Trp        | GCT<br>Ala        | AAG<br>Lys        | GTT<br>Val<br>255 | TTG<br>Leu<br>255 | GTT<br>Val        | 768 |
| GTG<br>Val        | ATG<br>Met        | CTA<br>Leu        | CTC<br>Leu | TTT<br>Phe<br>260 | GCC<br>Ala        | GGC<br>Gly        | GTC<br>Val        | GAC<br>Asp<br>265 | GGG<br>Gly        | CAT<br>His        | ACC<br>Thr        | CGC<br>Arg        | GTG<br>Val<br>270 | TCA<br>Ser        | GGA<br>Gly        | 816 |
| GGG<br>Gly        | GCA<br>Ala        | GCA<br>Ala        | GCC<br>Ala | TCC<br>Ser        | GAT<br>Asp        | ACC<br>Thr        | AGG<br>Arg        | GGC<br>Gly        | CTT<br>Leu        | GTG<br>Val        | TCC<br>Ser        | CTC<br>Leu        | TTT<br>Phe        | AGC<br>Ser        | CCC<br>Pro        | 864 |

| 275               |            |            |            |            | 280        |            |            |            |            | 285        |            |            |            |            |            |      |
|-------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| GGG<br>Gly<br>290 | TCG<br>Ser | GCT<br>Ala | CAG<br>Gln | AAA<br>Lys | ATC<br>Ile | CAG<br>Gln | CTC<br>Leu | GTA<br>Val | AAC<br>Asn | ACC<br>Thr | AAC<br>Asn | GGC<br>Gly | AGT<br>Ser | TGG<br>Trp | CAC<br>His | 912  |
| ATC<br>Ile<br>305 | AAC<br>Asn | AGG<br>Arg | ACT<br>Thr | GCC<br>Ala | CTG<br>Leu | AAC<br>Asn | TGC<br>Cys | AAC<br>Asn | GAC<br>Asp | TCC<br>Ser | CTC<br>Leu | CAA<br>Gln | ACA<br>Thr | GGG<br>Gly | TTC<br>Phe | 960  |
| TTT<br>Phe        | GCC<br>Ala | GCA<br>Ala | CTA<br>Leu | TTC<br>Phe | TAC<br>Tyr | AAA<br>Lys | CAC<br>His | AAA<br>Lys | TTC<br>Phe | AAC<br>Asn | TCG<br>Ser | TCT<br>Ser | GGA<br>Gly | TGC<br>Cys | CCA<br>Pro | 1008 |
| GAG<br>Glu        | CGC<br>Arg | TTG<br>Leu | GCC<br>Ala | AGC<br>Ser | TGT<br>Cys | CGC<br>Arg | TCC<br>Ser | ATC<br>Ile | GAC<br>Asp | AAG<br>Lys | TTC<br>Phe | GCT<br>Ala | CAG<br>Gln | GGG<br>Gly | TGG<br>Trp | 1056 |
| GGT<br>Gly        | CCC<br>Pro | CTC<br>Leu | ACT<br>Thr | TAC<br>Tyr | ACT<br>Thr | GAG<br>Glu | CCT<br>Pro | AAC<br>Asn | AGC<br>Ser | TCG<br>Ser | GAC<br>Asp | CAG<br>Gln | AGG<br>Arg | CCC<br>Pro | TAC<br>Tyr | 1104 |
| TGC<br>Cys        | TGG<br>Trp | CAC<br>His | TAC<br>Tyr | GCG<br>Ala | CCT<br>Pro | CGA<br>Arg | CCG<br>Pro | TGT<br>Cys | GGT<br>Gly | ATT<br>Ile | GTA<br>Val | CCC<br>Pro | GCG<br>Ala | TCT<br>Ser | CAG<br>Gln | 1152 |
| GTG<br>Val<br>385 | TGC<br>Cys | GGT<br>Gly | CCA<br>Pro | GTG<br>Val | TAT<br>Tyr | TGC<br>Cys | TTC<br>Phe | ACC<br>Thr | CCG<br>Pro | AGC<br>Ser | CCT<br>Pro | GTT<br>Val | GTG<br>Val | GTG<br>Val | GGG<br>Gly | 1200 |
| ACG<br>Thr        | ACC<br>Thr | GAT<br>Asp | CGG<br>Arg | TTT<br>Phe | GGT<br>Gly | GTC<br>Val | CCC<br>Pro | ACG<br>Thr | TAT<br>Tyr | AAC<br>Asn | TGG<br>Trp | GGG<br>Gly | GCG<br>Ala | AAC<br>Asn | GAC<br>Asp | 1248 |
| TCG<br>Ser        | GAT<br>Asp | GTG<br>Val | CTG<br>Leu | ATT<br>Ile | CTC<br>Leu | AAC<br>Asn | AAC<br>Asn | ACG<br>Thr | CGG<br>Arg | CCG<br>Pro | CCG<br>Pro | CGA<br>Arg | GGC<br>Gly | AAC<br>Asn | TGG<br>Trp | 1296 |
| TTC<br>Phe        | GGC<br>Gly | TGT<br>Cys | ACA<br>Thr | TGG<br>Trp | ATG<br>Met | AAT<br>Asn | GGC<br>Gly | ACT<br>Thr | GGG<br>Gly | TTC<br>Phe | ACC<br>Thr | AAG<br>Lys | ACG<br>Thr | TGT<br>Cys | GGG<br>Gly | 1344 |
| GGC<br>Gly        | CCC<br>Pro | CCG<br>Pro | TGC<br>Cys | AAC<br>Asn | ATC<br>Ile | GGG<br>Gly | GGG<br>Gly | GCC<br>Ala | GGC<br>Gly | AAC<br>Asn | AAC<br>Asn | ACC<br>Thr | TTG<br>Leu | ACC<br>Thr | TGC<br>Cys | 1392 |
| CCC<br>Pro<br>465 | ACT<br>Thr | GAC<br>Asp | TGT<br>Cys | TTT<br>Phe | CGG<br>Arg | AAG<br>Lys | CAC<br>His | CCC<br>Pro | GAG<br>Glu | GCC<br>Ala | ACC<br>Thr | TAC<br>Tyr | GCC<br>Ala | AGA<br>Arg | TGC<br>Cys | 1440 |
| GGT<br>Gly        | TCT<br>Ser | GGG<br>Gly | CCC<br>Pro | TGG<br>Trp | CTG<br>Leu | ACA<br>Thr | CCT<br>Pro | AGG<br>Arg | TGT<br>Cys | ATG<br>Met | GTT<br>Val | CAT<br>His | TAC<br>Tyr | CCA<br>Pro | TAT<br>Tyr | 1488 |
| AGG<br>Arg        | CTC<br>Leu | TGG<br>Trp | CAC<br>His | TAC<br>Tyr | CCC<br>Pro | TGC<br>Cys | ACT<br>Thr | GTC<br>Val | AAC<br>Asn | TTC<br>Phe | ACC<br>Thr | ATC<br>Ile | TTC<br>Phe | AAG<br>Lys | GTT<br>Val | 1536 |
| AGG<br>Arg        | ATG<br>Met | TAC<br>Tyr | GTG<br>Val | GGG<br>Gly | GGC<br>Gly | GTG<br>Val | GAG<br>Glu | CAC<br>His | AGG<br>Arg | TTC<br>Phe | GAA<br>Glu | GCC<br>Ala | GCA<br>Ala | TGC<br>Cys | AAT<br>Asn | 1584 |
| TGG               | ACT        | CGA        | GGA        | GAG        | CGT        | TGT        | GAC        | TTG        | GAG        | GAC        | AGG        | GAT        | AGA        | TCA        | GAG        | 1632 |

|     |     |     |     |        |     |     |     |     |     |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Trp | Thr | Arg | Gly | Glu    | Arg | Cys | Asp | Leu | Glu | Asp | Arg | Asp | Arg | Ser | Glu |      |  |
| 530 |     |     |     |        |     | 535 |     |     |     |     | 540 |     |     |     |     |      |  |
| CTT | AGC | CCG | CTG | CTG    | CTG | TCT | ACA | ACA | GAG | TGG | CAG | ATA | CTG | CCC | TGT | 1680 |  |
| Leu | Ser | Pro | Leu | Leu    | Leu | Ser | Thr | Thr | Glu | Trp | Gln | Ile | Leu | Pro | Cys |      |  |
| 545 |     |     |     |        | 550 |     |     |     |     | 555 |     |     |     |     | 560 |      |  |
| TCC | TTC | ACC | ACC | CTG    | CCG | GCC | CTA | TCC | ACC | GGC | CTG | ATC | CAC | CTC | CAT | 1728 |  |
| Ser | Phe | Thr | Thr | Leu    | Pro | Ala | Leu | Ser | Thr | Gly | Leu | Ile | His | Leu | His |      |  |
|     |     |     |     | 565    |     |     |     |     | 570 |     |     |     |     | 575 |     |      |  |
| CAG | AAC | ATC | GTG | GAC    | GTG | CAA | TAC | CTG | TAC | GGT | GTA | GGG | TCG | GCG | GTT | 1776 |  |
| Gln | Asn | Ile | Val | Asp    | Val | Gln | Tyr | Leu | Tyr | Gly | Val | Gly | Ser | Ala | Val |      |  |
|     |     |     | 580 |        |     |     |     | 585 |     |     |     |     | 590 |     |     |      |  |
| GTC | TCC | CTT | GTC | ATC    | AAA | TGG | GAG | TAT | GTC | CTG | TTG | CTC | TTC | CTT | CTC | 1824 |  |
| Val | Ser | Leu | Val | Ile    | Lys | Trp | Glu | Tyr | Val | Leu | Leu | Leu | Phe | Leu | Leu |      |  |
|     |     | 595 |     |        |     |     | 600 |     |     |     |     | 605 |     |     |     |      |  |
| CTG | GCA | GAC | GCG | CGC    | ATC | TGC | GCC | TGC | TTA | TGG | ATG | ATG | CTG | CTG | ATA | 1872 |  |
| Leu | Ala | Asp | Ala | Arg    | Ile | Cys | Ala | Cys | Leu | Trp | Met | Met | Leu | Leu | Ile |      |  |
|     | 610 |     |     |        |     | 615 |     |     |     |     | 620 |     |     |     |     |      |  |
| GCT | CAA | GCT | GAG | GCC    | GCC | TTA | GAG | AAC | CTG | GTG | GTC | CTC | AAT | GCG | GCG | 1920 |  |
| Ala | Gln | Ala | Glu | Ala    | Ala | Leu | Glu | Asn | Leu | Val | Val | Leu | Asn | Ala | Ala |      |  |
| 625 |     |     |     |        | 630 |     |     |     | 635 |     |     |     |     |     | 640 |      |  |
| GCC | GTG | GCC | GGG | GCG    | CAT | GGC | ACT | CTT | TCC | TTC | CTT | GTG | TTC | TTC | TGT | 1968 |  |
| Ala | Val | Ala | Gly | Ala    | His | Gly | Thr | Leu | Ser | Phe | Leu | Val | Phe | Phe | Cys |      |  |
|     |     |     |     | 645    |     |     |     |     | 650 |     |     |     |     | 655 |     |      |  |
| GCT | GCC | TGG | TAC | ATC    | AAG | GGC | AGG | CTG | GTC | CCT | GGT | GCG | GCA | TAC | GCC | 2016 |  |
| Ala | Ala | Trp | Tyr | Ile    | Lys | Gly | Arg | Leu | Val | Pro | Gly | Ala | Ala | Tyr | Ala |      |  |
|     |     |     | 660 |        |     |     |     | 665 |     |     |     |     | 670 |     |     |      |  |
| TTC | TAT | GGC | GTG | TGG    | CCG | CTG | CTC | CTG | CTT | CTG | CTG | GCC | TTA | CCA | CCA | 2064 |  |
| Phe | Tyr | Gly | Val | Trp    | Pro | Leu | Leu | Leu | Leu | Leu | Leu | Ala | Leu | Pro | Pro |      |  |
|     |     | 675 |     |        |     | 680 |     |     |     |     |     | 685 |     |     |     |      |  |
| CGA | GCT | TAT | GCC | TAGTAA |     |     |     |     |     |     |     |     |     |     |     | 2082 |  |
| Arg | Ala | Tyr | Ala |        |     |     |     |     |     |     |     |     |     |     |     |      |  |
|     |     |     | 690 |        |     |     |     |     |     |     |     |     |     |     |     |      |  |

## (2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 692 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |

| 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |
|     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ala | Ala | Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Asp | Leu | Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys | Ser | Ala | Met | Tyr | Val |
|     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Gly | Asp | Leu | Cys | Gly | Ser | Val | Phe | Leu | Val | Ser | Gln | Leu | Phe | Thr | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Pro | Arg | Arg | His | Glu | Thr | Val | Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Gly | His | Ile | Thr | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Trp | Ser | Pro | Thr | Thr | Ala | Leu | Val | Val | Ser | Gln | Leu | Leu | Arg | Ile | Pro |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val | Leu | Ala |
|     |     |     |     | 230 |     |     |     |     |     |     | 235 |     |     |     | 240 |
| Gly | Leu | Ala | Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp | Ala | Lys | Val | Leu | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Met | Leu | Leu | Phe | Ala | Gly | Val | Asp | Gly | His | Thr | Arg | Val | Ser | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Ala | Ala | Ala | Ser | Asp | Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe | Ser | Pro |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Ser | Ala | Gln | Lys | Ile | Gln | Leu | Val | Asn | Thr | Asn | Gly | Ser | Trp | His |
|     |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Asn | Arg | Thr | Ala | Leu | Asn | Cys | Asn | Asp | Ser | Leu | Gln | Thr | Gly | Phe |
|     |     |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |
| Phe | Ala | Ala | Leu | Phe | Tyr | Lys | His | Lys | Phe | Asn | Ser | Ser | Gly | Cys | Pro |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Glu | Arg | Leu | Ala | Ser | Cys | Arg | Ser | Ile | Asp | Lys | Phe | Ala | Gln | Gly | Trp |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gly | Pro | Leu | Thr | Tyr | Thr | Glu | Pro | Asn | Ser | Ser | Asp | Gln | Arg | Pro | Tyr |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Cys | Trp | His | Tyr | Ala | Pro | Arg | Pro | Cys | Gly | Ile | Val | Pro | Ala | Ser | Gln |

[illegible]

## (2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2433 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..2430

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..2427

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC | 48  |
| Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn |     |
| 1 5 10 15                                                       |     |
| CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGT | 96  |
| Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly |     |
| 20 25 30                                                        |     |
| GGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG | 144 |
| Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala |     |
| 35 40 45                                                        |     |
| ACT AGG AAG ACT TCC GAG CGG TCG CAA CCT CGT GGG AGG CGA CAA CCT | 192 |
| Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro |     |
| 50 55 60                                                        |     |
| ATC CCC AAG GCT CGC CGA CCC GAG GGT AGG GCC TGG GCT CAG CCC GGG | 240 |
| Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly |     |
| 65 70 75 80                                                     |     |
| TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG GGG TGG GCA GGA TGG | 288 |
| Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp |     |
| 85 90 95                                                        |     |
| CTC CTG TCA CCC CGC GGC TCT CGG CCT AGT TGG GGC CCT ACA GAC CCC | 336 |
| Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro |     |
| 100 105 110                                                     |     |
| CGG CGT AGG TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC | 384 |
| Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys |     |
| 115 120 125                                                     |     |
| GGC TTC GCC GAC CTC GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA | 432 |
| Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu |     |
| 130 135 140                                                     |     |
| GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC | 480 |



|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| Gly<br>145 | Gly        | Ala        | Ala        | Arg        | Ala<br>150 | Leu        | Ala        | His        | Gly        | Val<br>155 | Arg        | Val        | Leu        | Glu        | Asp<br>160 |      |
| GGC<br>Gly | GTG<br>Val | AAC<br>Asn | TAT<br>Tyr | GCA<br>Ala | ACA<br>Thr | GGG<br>Gly | AAT<br>Asn | TTG<br>Leu | CCC<br>Pro | GGT<br>Gly | TGC<br>Cys | TCT<br>Ser | TTC<br>Phe | TCT<br>Ser | ATC<br>Ile | 528  |
| TTC<br>Phe | CTC<br>Leu | TTG<br>Leu | GCT<br>Ala | TTG<br>Leu | CTG<br>Leu | TCC<br>Ser | TGT<br>Cys | CTG<br>Leu | ACC<br>Thr | GTT<br>Val | CCA<br>Pro | GCT<br>Ala | TCC<br>Ser | GCT<br>Ala | TAT<br>Tyr | 576  |
| GAA<br>Glu | GTG<br>Val | CGC<br>Arg | AAC<br>Asn | GTG<br>Val | TCC<br>Ser | GGG<br>Gly | ATG<br>Met | TAC<br>Tyr | CAT<br>His | GTC<br>Val | ACG<br>Thr | AAC<br>Asn | GAC<br>Asp | TGC<br>Cys | TCC<br>Ser | 624  |
| AAC<br>Asn | TCA<br>Ser | AGC<br>Ser | ATT<br>Ile | GTG<br>Val | TAT<br>Tyr | GAG<br>Glu | GCA<br>Ala | GCG<br>Ala | GAC<br>Asp | ATG<br>Met | ATC<br>Ile | ATG<br>Met | CAC<br>His | ACC<br>Thr | CCC<br>Pro | 672  |
| GGG<br>Gly | TGC<br>Cys | GTG<br>Val | CCC<br>Pro | TGC<br>Cys | GTT<br>Val | CGG<br>Arg | GAG<br>Glu | AAC<br>Asn | AAC<br>Asn | TCT<br>Ser | TCC<br>Ser | CGC<br>Arg | TGC<br>Cys | TGG<br>Trp | GTA<br>Val | 720  |
| GCG<br>Ala | CTC<br>Leu | ACC<br>Thr | CCC<br>Pro | ACG<br>Thr | CTC<br>Leu | GCA<br>Ala | GCT<br>Ala | AGG<br>Arg | AAC<br>Asn | GCC<br>Ala | AGC<br>Ser | GTC<br>Val | CCC<br>Pro | ACC<br>Thr | ACG<br>Thr | 768  |
| ACA<br>Thr | ATA<br>Ile | CGA<br>Arg | CGC<br>Arg | CAC<br>His | GTC<br>Val | GAT<br>Asp | TTG<br>Leu | CTC<br>Leu | GTT<br>Val | GGG<br>Gly | GCG<br>Ala | GCT<br>Ala | GCT<br>Ala | TTC<br>Phe | TGT<br>Cys | 816  |
| TCC<br>Ser | GCT<br>Ala | ATG<br>Met | TAC<br>Tyr | GTG<br>Val | GGG<br>Gly | GAC<br>Asp | CTC<br>Leu | TGC<br>Cys | GGA<br>Gly | TCT<br>Ser | GTC<br>Val | TTC<br>Phe | CTC<br>Leu | GTC<br>Val | TCC<br>Ser | 864  |
| CAG<br>Gln | CTG<br>Leu | TTC<br>Phe | ACC<br>Thr | ATC<br>Ile | TCG<br>Ser | CCT<br>Pro | CGC<br>Arg | CGG<br>Arg | CAT<br>His | GAG<br>Glu | ACG<br>Thr | GTG<br>Val | CAG<br>Gln | GAC<br>Asp | TGC<br>Cys | 912  |
| AAT<br>Asn | TGC<br>Cys | TCA<br>Ser | ATC<br>Ile | TAT<br>Tyr | CCC<br>Pro | GGC<br>Gly | CAC<br>His | ATA<br>Ile | ACG<br>Thr | GGT<br>Gly | CAC<br>His | CGT<br>Arg | ATG<br>Met | GCT<br>Ala | TGG<br>Trp | 960  |
| GAT<br>Asp | ATG<br>Met | ATG<br>Met | ATG<br>Met | AAC<br>Asn | TGG<br>Trp | TCG<br>Ser | CCT<br>Pro | ACA<br>Thr | ACG<br>Thr | GCC<br>Ala | CTG<br>Leu | GTG<br>Val | GTA<br>Val | TCG<br>Ser | CAG<br>Gln | 1008 |
| CTG<br>Leu | CTC<br>Leu | CGG<br>Arg | ATC<br>Ile | CCA<br>Pro | CAA<br>Gln | GCT<br>Ala | GTC<br>Val | GTG<br>Val | GAC<br>Asp | ATG<br>Met | GTG<br>Val | GCG<br>Ala | GGG<br>Gly | GCC<br>Ala | CAT<br>His | 1056 |
| TGG<br>Trp | GGA<br>Gly | GTC<br>Val | CTG<br>Leu | GCG<br>Ala | GGC<br>Gly | CTC<br>Leu | GCC<br>Ala | TAC<br>Tyr | TAT<br>Tyr | TCC<br>Ser | ATG<br>Met | GTG<br>Val | GGG<br>Gly | AAC<br>Asn | TGG<br>Trp | 1104 |
| GCT<br>Ala | AAG<br>Lys | GTT<br>Val | TTG<br>Leu | GTT<br>Val | GTG<br>Val | ATG<br>Met | CTA<br>Leu | CTC<br>Leu | TTT<br>Phe | GCC<br>Ala | GGC<br>Gly | GTC<br>Val | GAC<br>Asp | GGG<br>Gly | CAT<br>His | 1152 |
| ACC<br>Thr | CGC<br>Arg | GTG<br>Val | TCA<br>Ser | GGA<br>Gly | GGG<br>Gly | GCA<br>Ala | GCA<br>Ala | GCC<br>Ala | TCC<br>Ser | GAT<br>Asp | ACC<br>Thr | AGG<br>Arg | GGC<br>Gly | CTT<br>Leu | GTG<br>Val | 1200 |

1152 1104 1008 960 912 864 816 768 720 672 624 576 528

|                   |                   |                   |                   |                   |                   |                   |                   |            |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| TCC<br>Ser        | CTC<br>Leu        | TTT<br>Phe        | AGC<br>Ser        | CCC<br>Pro<br>405 | GGG<br>Gly        | TCG<br>Ser        | GCT<br>Ala        | CAG<br>Gln | AAA<br>Lys<br>410 | ATC<br>Ile        | CAG<br>Gln        | CTC<br>Leu        | GTA<br>Val        | AAC<br>Asn<br>415 | ACC<br>Thr        | 1248 |
| AAC<br>Asn        | GGC<br>Gly        | AGT<br>Ser        | TGG<br>Trp<br>420 | CAC<br>His        | ATC<br>Ile        | AAC<br>Asn        | AGG<br>Arg        | ACT<br>Thr | GCC<br>Ala<br>425 | CTG<br>Leu        | AAC<br>Asn        | TGC<br>Cys        | AAC<br>Asn<br>430 | GAC<br>Asp        | TCC<br>Ser        | 1296 |
| CTC<br>Leu        | CAA<br>Gln        | ACA<br>Thr<br>435 | GGG<br>Gly        | TTC<br>Phe        | TTT<br>Phe        | GCC<br>Ala        | GCA<br>Ala<br>440 | CTA<br>Leu | TTC<br>Phe        | TAC<br>Tyr        | AAA<br>Lys        | CAC<br>His<br>445 | AAA<br>Lys        | TTC<br>Phe        | AAC<br>Asn        | 1344 |
| TCG<br>Ser        | TCT<br>Ser        | GGA<br>Gly<br>450 | TGC<br>Cys        | CCA<br>Pro        | GAG<br>Glu        | CGC<br>Arg<br>455 | TTG<br>Leu        | GCC<br>Ala | AGC<br>Ser        | TGT<br>Cys        | CGC<br>Arg<br>460 | TCC<br>Ser        | ATC<br>Ile        | GAC<br>Asp        | AAG<br>Lys        | 1392 |
| TTC<br>Phe<br>465 | GCT<br>Ala        | CAG<br>Gln        | GGG<br>Gly        | TGG<br>Trp        | GGT<br>Gly<br>470 | CCC<br>Pro        | CTC<br>Leu        | ACT<br>Thr | TAC<br>Tyr        | ACT<br>Thr        | GAG<br>Glu<br>475 | CCT<br>Pro        | AAC<br>Asn        | AGC<br>Ser        | TCG<br>Ser<br>480 | 1440 |
| GAC<br>Asp        | CAG<br>Gln        | AGG<br>Arg        | CCC<br>Pro        | TAC<br>Tyr<br>485 | TGC<br>Cys        | TGG<br>Trp        | CAC<br>His        | TAC<br>Tyr | GCG<br>Ala<br>490 | CCT<br>Pro        | CGA<br>Arg        | CCG<br>Pro        | TGT<br>Cys        | GGT<br>Gly<br>495 | ATT<br>Ile        | 1488 |
| GTA<br>Val        | CCC<br>Pro        | GCG<br>Ala        | TCT<br>Ser<br>500 | CAG<br>Gln        | GTG<br>Val        | TGC<br>Cys        | GGT<br>Gly<br>505 | CCA<br>Pro | GTG<br>Val        | TAT<br>Tyr        | TGC<br>Cys        | TTC<br>Phe<br>510 | ACC<br>Thr        | CCG<br>Pro        | AGC<br>Ser        | 1536 |
| CCT<br>Pro        | GTT<br>Val        | GTG<br>Val<br>515 | GTG<br>Val        | GGG<br>Gly        | ACG<br>Thr        | ACC<br>Thr        | GAT<br>Asp<br>520 | CGG<br>Arg | TTT<br>Phe        | GGT<br>Gly        | GTC<br>Val<br>525 | CCC<br>Pro        | ACG<br>Thr        | TAT<br>Tyr        | AAC<br>Asn        | 1584 |
| TGG<br>Trp<br>530 | GGG<br>Gly        | GCG<br>Ala        | AAC<br>Asn        | GAC<br>Asp        | TCG<br>Ser        | GAT<br>Asp<br>535 | GTG<br>Val        | CTG<br>Leu | ATT<br>Ile        | CTC<br>Leu        | AAC<br>Asn<br>540 | AAC<br>Asn        | ACG<br>Thr        | CGG<br>Arg        | CCG<br>Pro        | 1632 |
| CCG<br>Pro<br>545 | CGA<br>Arg        | GGC<br>Gly        | AAC<br>Asn        | TGG<br>Trp        | TTC<br>Phe<br>550 | GGC<br>Gly        | TGT<br>Cys        | ACA<br>Thr | TGG<br>Trp        | ATG<br>Met<br>555 | AAT<br>Asn        | GGC<br>Gly        | ACT<br>Thr        | GGG<br>Gly        | TTC<br>Phe<br>560 | 1680 |
| ACC<br>Thr        | AAG<br>Lys        | ACG<br>Thr        | TGT<br>Cys        | GGG<br>Gly<br>565 | GGC<br>Gly        | CCC<br>Pro        | CCG<br>Pro        | TGC<br>Cys | AAC<br>Asn<br>570 | ATC<br>Ile        | GGG<br>Gly        | GGG<br>Gly        | GCC<br>Ala        | GGC<br>Gly<br>575 | AAC<br>Asn        | 1728 |
| AAC<br>Asn        | ACC<br>Thr        | TTG<br>Leu<br>580 | ACC<br>Thr        | TGC<br>Cys        | CCC<br>Pro        | ACT<br>Thr        | GAC<br>Asp        | TGT<br>Cys | TTT<br>Phe<br>585 | CGG<br>Arg        | AAG<br>Lys        | CAC<br>His<br>590 | CCC<br>Pro        | GAG<br>Glu        | GCC<br>Ala        | 1776 |
| ACC<br>Thr        | TAC<br>Tyr        | GCC<br>Ala<br>595 | AGA<br>Arg        | TGC<br>Cys        | GGT<br>Gly        | TCT<br>Ser        | GGG<br>Gly<br>600 | CCC<br>Pro | TGG<br>Trp        | CTG<br>Leu        | ACA<br>Thr        | CCT<br>Pro<br>605 | AGG<br>Arg        | TGT<br>Cys        | ATG<br>Met        | 1824 |
| GTT<br>Val        | CAT<br>His<br>610 | TAC<br>Tyr        | CCA<br>Pro        | TAT<br>Tyr        | AGG<br>Arg        | CTC<br>Leu<br>615 | TGG<br>Trp        | CAC<br>His | TAC<br>Tyr        | CCC<br>Pro        | TGC<br>Cys<br>620 | ACT<br>Thr        | GTC<br>Val        | AAC<br>Asn        | TTC<br>Phe        | 1872 |
| ACC<br>Thr<br>625 | ATC<br>Ile        | TTC<br>Phe        | AAG<br>Lys        | GTT<br>Val        | AGG<br>Arg<br>630 | ATG<br>Met        | TAC<br>Tyr        | GTG<br>Val | GGG<br>Gly<br>635 | GGC<br>Gly        | GTG<br>Val        | GAG<br>Glu        | CAC<br>His        | AGG<br>Arg        | TTC<br>Phe<br>640 | 1920 |
| GAA               | GCC               | GCA               | TGC               | AAT               | TGG               | ACT               | CGA               | GGA        | GAG               | CGT               | TGT               | GAC               | TTG               | GAG               | GAC               | 1968 |

|     |     |     |     |     |     |     |     |     |        |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|--------|-----|-----|-----|-----|-----|-----|------|--|
| Glu | Ala | Ala | Cys | Asn | Trp | Thr | Arg | Gly | Glu    | Arg | Cys | Asp | Leu | Glu | Asp |      |  |
|     |     |     |     | 645 |     |     |     |     | 650    |     |     |     |     | 655 |     |      |  |
| AGG | GAT | AGA | TCA | GAG | CTT | AGC | CCG | CTG | CTG    | CTG | TCT | ACA | ACA | GAG | TGG | 2016 |  |
| Arg | Asp | Arg | Ser | Glu | Leu | Ser | Pro | Leu | Leu    | Leu | Ser | Thr | Thr | Glu | Trp |      |  |
|     |     |     | 660 |     |     |     |     | 665 |        |     |     |     |     | 670 |     |      |  |
| CAG | ATA | CTG | CCC | TGT | TCC | TTC | ACC | ACC | CTG    | CCG | GCC | CTA | TCC | ACC | GGC | 2064 |  |
| Gln | Ile | Leu | Pro | Cys | Ser | Phe | Thr | Thr | Leu    | Pro | Ala | Leu | Ser | Thr | Gly |      |  |
|     |     |     | 675 |     |     |     | 680 |     |        |     |     | 685 |     |     |     |      |  |
| CTG | ATC | CAC | CTC | CAT | CAG | AAC | ATC | GTG | GAC    | GTG | CAA | TAC | CTG | TAC | GGT | 2112 |  |
| Leu | Ile | His | Leu | His | Gln | Asn | Ile | Val | Asp    | Val | Gln | Tyr | Leu | Tyr | Gly |      |  |
|     |     |     | 690 |     |     | 695 |     |     |        |     | 700 |     |     |     |     |      |  |
| GTA | GGG | TCG | GCG | GTT | GTC | TCC | CTT | GTC | ATC    | AAA | TGG | GAG | TAT | GTC | CTG | 2160 |  |
| Val | Gly | Ser | Ala | Val | Val | Ser | Leu | Val | Ile    | Lys | Trp | Glu | Tyr | Val | Leu |      |  |
|     | 705 |     |     |     | 710 |     |     |     |        | 715 |     |     |     |     | 720 |      |  |
| TTG | CTC | TTC | CTT | CTC | CTG | GCA | GAC | GCG | CGC    | ATC | TGC | GCC | TGC | TTA | TGG | 2208 |  |
| Leu | Leu | Phe | Leu | Leu | Ala | Asp | Ala | Arg | Ile    | Cys | Ala | Cys | Leu | Trp |     |      |  |
|     |     |     |     | 725 |     |     |     | 730 |        |     |     |     |     | 735 |     |      |  |
| ATG | ATG | CTG | CTG | ATA | GCT | CAA | GCT | GAG | GCC    | GCC | TTA | GAG | AAC | CTG | GTG | 2256 |  |
| Met | Met | Leu | Leu | Ile | Ala | Gln | Ala | Glu | Ala    | Ala | Leu | Glu | Asn | Leu | Val |      |  |
|     |     |     |     | 740 |     |     |     | 745 |        |     |     |     | 750 |     |     |      |  |
| GTC | CTC | AAT | GCG | GCG | GCC | GTG | GCC | GGG | GCG    | CAT | GGC | ACT | CTT | TCC | TTC | 2304 |  |
| Val | Leu | Asn | Ala | Ala | Ala | Val | Ala | Gly | Ala    | His | Gly | Thr | Leu | Ser | Phe |      |  |
|     |     | 755 |     |     |     |     | 760 |     |        |     |     | 765 |     |     |     |      |  |
| CTT | GTG | TTC | TTC | TGT | GCT | GCC | TGG | TAC | ATC    | AAG | GGC | AGG | CTG | GTC | CCT | 2352 |  |
| Leu | Val | Phe | Phe | Cys | Ala | Ala | Trp | Tyr | Ile    | Lys | Gly | Arg | Leu | Val | Pro |      |  |
|     |     | 770 |     |     |     | 775 |     |     |        |     | 780 |     |     |     |     |      |  |
| GGT | GCG | GCA | TAC | GCC | TTC | TAT | GGC | GTG | TGG    | CCG | CTG | CTC | CTG | CTT | CTG | 2400 |  |
| Gly | Ala | Ala | Tyr | Ala | Phe | Tyr | Gly | Val | Trp    | Pro | Leu | Leu | Leu | Leu | Leu |      |  |
|     | 785 |     |     |     | 790 |     |     |     | 795    |     |     |     |     |     | 800 |      |  |
| CTG | GCC | TTA | CCA | CCA | CGA | GCT | TAT | GCC | TAGTAA |     |     |     |     |     |     | 2433 |  |
| Leu | Ala | Leu | Pro | Pro | Arg | Ala | Tyr | Ala |        |     |     |     |     |     |     |      |  |
|     |     |     |     | 805 |     |     |     | 810 |        |     |     |     |     |     |     |      |  |

## (2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 809 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Ser | Thr | Asn | Pro | Lys | Pro | Gln | Arg | Lys | Thr | Lys | Arg | Asn | Thr | Asn |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Arg | Arg | Pro | Gln | Asp | Val | Lys | Phe | Pro | Gly | Gly | Gly | Gln | Ile | Val | Gly |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Gly | Val | Tyr | Leu | Leu | Pro | Arg | Arg | Gly | Pro | Arg | Leu | Gly | Val | Arg | Ala |  |  |

| 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Arg | Lys | Thr | Ser | Glu | Arg | Ser | Gln | Pro | Arg | Gly | Arg | Arg | Gln | Pro |
| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ile | Pro | Lys | Ala | Arg | Arg | Pro | Glu | Gly | Arg | Ala | Trp | Ala | Gln | Pro | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Tyr | Pro | Trp | Pro | Leu | Tyr | Gly | Asn | Glu | Gly | Met | Gly | Trp | Ala | Gly | Trp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Leu | Ser | Pro | Arg | Gly | Ser | Arg | Pro | Ser | Trp | Gly | Pro | Thr | Asp | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Arg | Arg | Ser | Arg | Asn | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Gly | Phe | Ala | Asp | Leu | Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Gly | Ala | Ala | Arg | Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Val | Asn | Tyr | Ala | Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Leu | Leu | Ala | Leu | Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Val | Arg | Asn | Val | Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Ser | Ser | Ile | Val | Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Cys | Val | Pro | Cys | Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ala | Leu | Thr | Pro | Thr | Leu | Ala | Ala | Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Ile | Arg | Arg | His | Val | Asp | Leu | Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Ala | Met | Tyr | Val | Gly | Asp | Leu | Cys | Gly | Ser | Val | Phe | Leu | Val | Ser |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gln | Leu | Phe | Thr | Ile | Ser | Pro | Arg | Arg | His | Glu | Thr | Val | Gln | Asp | Cys |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asn | Cys | Ser | Ile | Tyr | Pro | Gly | His | Ile | Thr | Gly | His | Arg | Met | Ala | Trp |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Asp | Met | Met | Met | Asn | Trp | Ser | Pro | Thr | Thr | Ala | Leu | Val | Val | Ser | Gln |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Leu | Arg | Ile | Pro | Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Trp | Gly | Val | Leu | Ala | Gly | Leu | Ala | Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ala | Lys | Val | Leu | Val | Val | Met | Leu | Le  |     |     |     |     |     |     |     |

| 370        |            |            |            |            | 375        |            |            |            |            | 380        |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Thr<br>385 | Arg        | Val        | Ser        | Gly        | Gly<br>390 | Ala        | Ala        | Ala        | Ser        | Asp<br>395 | Thr        | Arg        | Gly        | Leu        | Val<br>400 |
| Ser        | Leu        | Phe        | Ser        | Pro<br>405 | Gly        | Ser        | Ala        | Gln        | Lys<br>410 | Ile        | Gln        | Leu        | Val        | Asn<br>415 | Thr        |
| Asn        | Gly        | Ser        | Trp<br>420 | His        | Ile        | Asn        | Arg        | Thr<br>425 | Ala        | Leu        | Asn        | Cys        | Asn<br>430 | Asp        | Ser        |
| Leu        | Gln        | Thr<br>435 | Gly        | Phe        | Phe        | Ala        | Ala<br>440 | Leu        | Phe        | Tyr        | Lys        | His<br>445 | Lys        | Phe        | Asn        |
| Ser        | Ser<br>450 | Gly        | Cys        | Pro        | Glu        | Arg<br>455 | Leu        | Ala        | Ser        | Cys        | Arg<br>460 | Ser        | Ile        | Asp        | Lys        |
| Phe<br>465 | Ala        | Gln        | Gly        | Trp        | Gly<br>470 | Pro        | Leu        | Thr        | Tyr        | Thr<br>475 | Glu        | Pro        | Asn        | Ser        | Ser<br>480 |
| Asp        | Gln        | Arg        | Pro        | Tyr<br>485 | Cys        | Trp        | His        | Tyr        | Ala<br>490 | Pro        | Arg        | Pro        | Cys        | Gly<br>495 | Ile        |
| Val        | Pro        | Ala        | Ser<br>500 | Gln        | Val        | Cys        | Gly<br>505 | Pro        | Val        | Tyr        | Cys        | Phe<br>510 | Thr        | Pro        | Ser        |
| Pro        | Val<br>515 | Val        | Val        | Gly        | Thr        | Thr        | Asp<br>520 | Arg        | Phe        | Gly        | Val        | Pro<br>525 | Thr        | Tyr        | Asn        |
| Trp<br>530 | Gly        | Ala        | Asn        | Asp        | Ser        | Asp<br>535 | Val        | Leu        | Ile        | Leu        | Asn<br>540 | Asn        | Thr        | Arg        | Pro        |
| Pro<br>545 | Arg        | Gly        | Asn        | Trp        | Phe<br>550 | Gly        | Cys        | Thr        | Trp        | Met<br>555 | Asn        | Gly        | Thr        | Gly        | Phe<br>560 |
| Thr        | Lys        | Thr        | Cys        | Gly<br>565 | Gly        | Pro        | Pro        | Cys        | Asn<br>570 | Ile        | Gly        | Gly        | Ala<br>575 | Gly        | Asn        |
| Asn        | Thr        | Leu        | Thr<br>580 | Cys        | Pro        | Thr        | Asp<br>585 | Cys        | Phe        | Arg        | Lys        | His<br>590 | Pro        | Glu        | Ala        |
| Thr        | Tyr<br>595 | Ala        | Arg        | Cys        | Gly        | Ser        | Gly<br>600 | Pro        | Trp        | Leu        | Thr<br>605 | Pro        | Arg        | Cys        | Met        |
| Val<br>610 | His        | Tyr        | Pro        | Tyr        | Arg        | Leu<br>615 | Trp        | His        | Tyr        | Pro        | Cys<br>620 | Thr        | Val        | Asn        | Phe        |
| Thr<br>625 | Ile        | Phe        | Lys        | Val        | Arg<br>630 | Met        | Tyr        | Val        | Gly        | Gly<br>635 | Val        | Glu        | His        | Arg        | Phe<br>640 |
| Glu        | Ala        | Ala        | Cys        | Asn<br>645 | Trp        | Thr        | Arg        | Gly        | Glu<br>650 | Arg        | Cys        | Asp        | Leu        | Glu<br>655 | Asp        |
| Arg        | Asp        | Arg        | Ser<br>660 | Glu        | Leu        | Ser        | Pro        | Leu<br>665 | Leu        | Leu        | Ser        | Thr<br>670 | Thr        | Glu        | Trp        |
| Gln        | Ile        | Leu        | Pro        | Cys        | Ser        | Phe        | Thr<br>680 | Thr        | Leu        | Pro        | Ala        | Leu<br>685 | Ser        | Thr        | Gly        |
| Leu<br>690 | Ile        | His        | Leu        | His        | Gln        | Asn<br>695 | Ile        | Val        | Asp        | Val        | Gln<br>700 | Tyr        | Leu        | Tyr        | Gly        |

Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu  
 705 710 715 720  
 Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp  
 725 730 735  
 Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val  
 740 745 750  
 Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe  
 755 760 765  
 Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro  
 770 775 780  
 Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu  
 785 790 795 800  
 Leu Ala Leu Pro Pro Arg Ala Tyr Ala  
 805

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 1..17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Ser Asn Ser Ser Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys  
 1 5 10 15  
 Val

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 1..22

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Gly Gly Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
 1 5 10 15

Ser Pro Thr Thr Ala Leu  
 20

## (2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site  
 (B) LOCATION: 1..37

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys  
 1 5 10 15

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr  
 20 25 30

Pro Gly Cys Gly Lys  
 35

## (2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site  
 (B) LOCATION: 1..25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gly Gly Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr  
 1 5 10 15

Gln Leu Arg Arg His Ile Asp Leu Leu  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:





## (2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala His Asp Ala Ile  
 1                      5                      10                      15  
 Leu His Thr Pro  
                     20

## (2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr  
 1                      5                      10                      15  
 Pro Gly Cys Val  
                     20

## (2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

His Asp Ala Ile Leu His Thr Pro Gly Val Pro Cys Val Arg Glu Gly  
 1                      5                      10                      15  
 Asn Val Ser

## (2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Cys Val Arg Glu Gly Asn Val Ser Arg Cys Trp Val Ala Met Thr Pro  
 1                      5                      10                      15  
 Thr Val Ala Thr  
                     20

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr  
 1                      5                      10                      15  
 Gln Leu Arg Arg  
                     20

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser  
 1                      5                      10                      15  
 Ala Thr Leu Cys  
                     20

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: peptide

Leu Val Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu  
1 5 10 15  
Cys Gly Ser Val  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr Thr Gln Gly Cys  
1 5 10 15  
Asn Cys Ser Ile  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His  
1 5 10 15  
Arg Met Ala Trp  
20

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

INFORMATION FOR SEQ ID NO: 68:

(ii) MOLECULE TYPE: peptide

Asn Trp Ser Pro Thr Ala Ala Leu Val Met Ala Gln Leu Leu Arg Ile  
1 5 10 15  
Pro Gln Ala Ile  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

Leu Leu Arg Ile Pro Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His  
1 5 10 15  
Trp Gly Val Leu  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met  
1 5 10 15  
Val Gly Asn Met  
20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala Glu Thr Ile Val Ser  
1 5 10 15  
Gly Gly Gln Ala  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Ser Gly Leu Val Ser Leu Phe Thr Pro Gly Ala Lys Gln Asn Ile Gln  
1 5 10 15  
Leu Ile Asn Thr  
20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Gln Asn Ile Gln Leu Ile Asn Thr Asn Gly Gln Trp His Ile Asn Ser  
1 5 10 15  
Thr Ala Leu Asn  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Leu Asn Cys Asn Glu Ser Leu Asn Thr Gly Trp Trp Leu Ala Gly Leu  
1 5 10 15  
Ile Tyr Gln His Lys  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Ala Gly Leu Ile Tyr Gln His Lys Phe Asn Ser Ser Gly Cys Pro Glu  
1 5 10 15  
Arg Leu Ala Ser  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Pro Leu Thr Asp Phe Asp

(2) INFORMATION FOR SEO ID NO: 77:

- (ii) MOLECULE TYPE: peptide

Gly Pro Asp Gln  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Pro Lys Pro Cys  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Cys Gly Pro Val

20

## (2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Lys | Ser | Val | Cys | Gly | Pro | Val | Tyr | Cys | Phe | Thr | Pro | Ser | Pro | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |
|-----|-----|-----|-----|
| Val | Val | Gly | Thr |
|     |     |     | 20  |

## (2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Pro | Val | Val | Val | Gly | Thr | Thr | Asp | Arg | Ser | Gly | Ala | Pro | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |
|-----|-----|-----|-----|
| Tyr | Ser | Trp | Gly |
|     |     |     | 20  |

## (2) INFORMATION FOR SEQ ID NO: 82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ala | Pro | Thr | Tyr | Ser | Trp | Gly | Glu | Asn | Asp | Thr | Asp | Val | Phe | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |
|-----|-----|-----|-----|
| Leu | Asn | Asn | Thr |
|     |     |     | 20  |

## (2) INFORMATION FOR SEQ ID NO: 83:



- (2) INFORMATION FOR SEQ ID NO: 86:

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Thr Asp Cys Phe Arg Lys His Pro Asp Ala Thr Tyr Ser Arg Cys Gly  
1                      5                      10                      15

Ser Gly Pro Trp  
20

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr Pro Arg Cys Leu Val Asp  
1                      5                      10                      15

Tyr Pro Tyr Arg  
20

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Ile  
1                      5                      10                      15

Asn Tyr Thr Ile  
20

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

(2) INFORMATION FOR SEQ ID NO: 90:

(ii) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Met Tyr Val Gly Gly Val Glu His Arg Leu Glu Ala Ala Cys Asn Trp  
1 5 10 15  
Thr Pro Gly Glu  
20

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Ala Cys Asn Trp Thr Pro Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp  
1 5 10 15  
Arg Ser Glu Leu  
20

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Thr Thr Thr  
 1 5 10 15  
 Gln Trp Gln Val  
 20

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Tyr Gln Val Arg Asn Ser Thr Gly Leu  
 1 5

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

ACGTCCGTAC GTTCGAATTA ATTAATCGA

29

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

CCTCCGGACG TGCCTAGCT CCCGTCTGTG GTAGTGGTGG TAGTGATTAT CAATTAATTG 60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CGTGACATGG TACATPCCGG ACACTTGGCG CACTTCATAA GCGGA

45

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

TGCCTCATAC ACAATGGAGC TCTGGGACGA GTCGTTCTGTG AC

42

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

TACCCAGCAG CGGGAGCTCT GTTGCTCCCG AACGCAGGGC AC

42

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

42

(iii) ANTI-SENSE: NO

48

(iii) ANTI-SENSE: NO

42

(iii) ANTI-SENSE: NO

26

## (2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:  
GCTCCATTGT GTATGAGGCA GCGG

24

## (2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:  
GAGCTCCCGC TGCTGGGTAG CGC

23

## (2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:  
CCTCCGTCCC CACCACGACA ATACG

25

## (2) INFORMATION FOR SEQ ID NO: 108:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CTACCCGGGC CACATAACGG GTCACCG

27

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GGAGGCCTAC AACGGCCCTG GTGG

24

(2) INFORMATION FOR SEQ ID NO: 110:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TTCTATCGAT TAAATAGAAT TC

22

(2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid

(iii) ANTI-SENSE: NO

GCCATACGCT CACAGCCGAT CCC

## (2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys  
 1                      5                      10                      15  
 Ser Asn Ser Ser  
                     20

## (2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp  
 1                      5                      10                      15  
 Met Ile Met His Thr  
                     20

## (2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val  
 1                      5                      10                      15

Arg Glu Asn Asn Ser  
20

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu  
 1 5 10 15

Thr Pro Thr Leu Ala  
 20

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro  
 1 5 10 15

Thr Thr Thr Ile Arg  
 20

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

|                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser                 | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His | Val | Asp | Leu | Leu | Val |
| 1                   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |
| Gly Ala Ala Ala Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 118:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

|                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu                 | Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys | Ser | Ala | Met | Tyr | Val | Gly |
| 1                   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |
| Asp Leu Cys Gly Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 119:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

|                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr                 | Val | Gly | Asp | Leu | Cys | Gly | Ser | Val | Phe | Leu | Val | Ser | Gln | Leu |
| 1                   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |
| Phe Thr Ile Ser Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

|                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser                 | Gln | Leu | Phe | Thr | Ile | Ser | Pro | Arg | Arg | His | Glu | Thr | Val | Gln |
| 1                   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |
| Asp Cys Asn Cys Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

|                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr                 | Val | Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr | Pro | Gly | His | Ile | Thr |
| 1                   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |
| Gly His Arg Met Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

|                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His                 | Ile | Thr | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn | Trp |
| 1                   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |
| Ser Pro Thr Thr Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |